

From: Mertz, Prema  
Sent: Monday, October 31, 2005 3:22 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/748,484

Please search SEQ ID NO:2 and any 6 amino acids of SEQ ID No:2 with protein databases.

Please search USGPUB databases with SEQ ID NO:2.

Thanks.

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aa

Mej 176

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

#### Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

#### Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ Other CAF

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 2, 2005, 18:32:00 ; Search time 40 Seconds

(without alignments)  
423.354 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 910

Sequence: 1 MKASSLAFSLSAFYLMT.....AVVKALGELDLILQMEETE .176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156.5	17.2	178	2 A38580	interleukin-10 pre
2	155	17.0	170	1 QOBR2	BCRF1 protein - hu
3	155	17.0	175	2 I46591	interleukin 10 - p
4	147.5	16.2	179	2 A48558	interleukin 10 hom
5	144	15.8	178	2 A34853	interleukin-10 pre
6	136	14.9	178	2 JN0475	interleukin-10 pre
7	94.5	10.4	567	2 JCS538	Rab geranylgeranyl
8	94.5	10.4	567	2 A45977	Rab geranylgeranyl
9	93.5	10.3	809	2 S64594	probable beta-adap
10	85	9.3	140	2 F83128	probable transcrip
11	81.5	9.0	146	2 T33346	hypothetical prote
12	81	8.9	1062	2 S46367	protein kinase CDC
13	80	8.8	542	2 T19925	hypothetical prote
14	76.5	8.4	502	2 AD3160	hypothetical prote
15	76.5	8.4	553	2 B90153	2-isoopropylmalate
16	76	8.4	523	2 S64826	probable membrane
17	76	8.4	917	2 T21870	hypothetical prote
18	75	8.2	276	2 B71517	probable synchocy
19	75	8.2	726	2 T48023	ATP-dependent RNA
20	75	8.2	729	2 H84912	probable pre-mRNA
21	74.5	8.2	121	2 E83640	hypothetical prote
22	74.5	8.2	1047	2 D71302	probable exonuclea
23	74	8.1	682	1 H69819	ATP-dependent DNA
24	73.5	8.1	449	2 B71917	udp-n-acetylmurama
25	73.5	8.1	653	2 D87602	sensory box histid
26	73.5	8.1	729	2 F97321	membrane export pr
27	73.5	8.1	782	2 S33945	late protein, 100K
28	73.5	8.1	794	2 A98211	hypothetical prote
29	73.5	8.1	794	2 C86057	hypothetical prote

30	73	8.0	471	2 B38637	Ras inhibitor (c1o
31	73	8.0	563	2 D90531	exonuclease ABC s
32	73	8.0	614	2 B93880	hypothetical prote
33	73	8.0	1008	2 D84434	probable receptor-
34	72.5	8.0	261	2 H98213	transcription repr
35	72.5	8.0	388	2 T00641	hypothetical prote
36	72.5	8.0	409	2 A54750	TNF receptor assoc
37	72.5	8.0	447	2 T20552	hypothetical prote
38	72.5	8.0	481	2 S38682	YmbL protein - Bac
39	72.5	8.0	1101	2 T33153	hypothetical prote
40	72.5	8.0	2182	2 T28634	variant-specific s
41	72.5	8.0	2581	2 AP2545	conserved hypotet
42	72	7.9	255	2 F81833	conserved hypotet
43	72	7.9	255	2 E81197	hypothetical prote
44	72	7.9	279	2 A70081	conserved hypotet
45	72	7.9	351	2 S74651	hypothetical prote

#### ALIGNMENTS

RESULT 1  
A38580  
Interleukin-10 precursor - human  
N:Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #ext\_change 09-Jul-2004  
C:Accession: A38580; G01539; S49110; I37890  
R:Vieth, P.; de Mail-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Fiorentino, Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991  
A:Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c1c  
A:Reference number: A38580; MUID:91142134; PMID:1847510  
A:Accession: A38580  
A:Molecule type: mRNA  
A:Residues: 1-178 <VIB>  
A:Cross-references: UNIPROT:P22301; GB:M57627; NID:g186270; PID:AAA63207.1; PID:g186271  
R:Rindor, W.T.; Syro, R.; Tsaribopolos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Pallwa1  
Biochemistry 32: 8807-8815, 1993  
A:Title: Disulfide bond assignments and secondary structure analysis of human and murin  
A:Reference number: A48693; MUID:93372085; PMID:8364028  
A:Contents: annotation; disulfide bonds in recombinant protein  
R:Sanjanwala, B.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: G07695  
A:Accession: G01539  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-178 <SAN>  
A:Cross-references: EMBL:U06720; NID:g1041812; PID:AAA80104.1; PID:g1041813  
R:Kube, D.; Platzer, C.; von Knechten, A.; Straub, H.; Hafner, M.; Tesch, H.  
submitted to the EMBL Data Library, March 1994  
A:Description: Isolation of the human interleukin-10-promoter. Characterization of the  
A:Reference number: S49110  
A:Accession: S49110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6, 'PVWSS' <KUB>  
A:Cross-references: EMBL:X78437; NID:g1167482  
R:Platzer, C.; Volk, H.D.; Platzer, M.  
DNA Seq. 4: 399-401, 1994  
A:Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walki  
A:Reference number: I37890; MUID:95143580; PMID:7841462  
A:Accession: I37890  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <PLA>  
A:Cross-references: EMBL:X73536; NID:g4523395; PID:CAA51942.1; PID:g580177  
C:Gene: GDB:1110; IL-10  
A:Cross-references: GDB:128636; OMIM:124092  
A:Map position: 1q31-1q32  
A:Introns: 55/3; 75/3; 126/3; 148/3  
C:Superfamily: interleukin-10

C:Keywords: cytokine; glycoprotein; lymphokine; T-cell  
F:1-18/Domains: signal sequence #status predicted <S>  
F:19-178/Product: interleukin-10 #status predicted <M>  
F:30-126,80-132/Dissulfide bonds: #status experimental  
F:134/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 17.2%; Score 156.5; DB 2; Length 178;  
Best Local Similarity 27.4%; Pred. No. 7.9e-08;  
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 5;  
QY 22 STGLTNLNGSCV-----IATNLOEIRNGFSDIRGSVOAKDGNIDIRLRTESLQDTKP 76  
DB 19 SPGQGTQSENSCTHPGMLPMLRLDRDAFSKVFQMKD-QLD-NLLKESLLEDFKG 76  
QY 77 ANRCCLLHLRLYLDRVFNKQTPDHTLRKISLANSFLTKKDLRLCHAMTCHGE 136  
DB 77 YLGCALSBEMIQFYLBVMPQANODPDIKAHVNSLGEKTLRLRRCRFLPC---E 133  
QY 137 BAMKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173  
DB 134 NKSRAVEQVKAFAFKLQ-EKGIYKAMSEFDIFINYIE 169

## RESULT 2

QOBR2  
BCRF1 protein - human herpesvirus 4 (strain B95-8)  
C:Species: human herpesvirus 4, Epstein-Barr virus  
C:Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 09-Jul-2004  
C:Accession: A03741; S32974  
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
Mol. Biol. Med. 1, 21-45, 1983  
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus  
A:Reference number: A33065; MUID:85035713; PMID:6092825  
A:Accession: A03741  
A:Molecule type: DNA  
A:Residues: 1-170 <BAN>  
A:Cross-references: UNIPROT:P03180; EMBL:V01555; NID:959074; PIDN:CAA24863.1; PID:959076  
R:Bankier, A.T.; Blyskal, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H  
Nature 310, 207-211, 1984  
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A:Reference number: A03794; MUID:84270667; PMID:6087149  
A:Contents: annotation; protein coding region  
C:Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 1; Length 170;  
Best Local Similarity 28.9%; Pred. No. 1e-07;  
Matches 39; Conservative 29; Mismatches 61; Indels 6; Gaps 4;  
QY 39 LOEIRNGFSDIRGSVOAKDGNIDIRLRTESLQDTKPANRCCLRLHLRLYLDRVFNKY 98  
DB 34 LRDLDAFSRVKTFQTKD-EVD-NLLKESLLEDFKGLGQALSEMIQFYLBVMPQA 91  
QY 99 QTPDHTLRKISLANSFLTKKDLRLCHAMTCHGEAMKYSQILSHFEKLEPQAAV 158  
DB 92 ENODPEAKDHNVSLOENKTLRLRLRRCRFLPC---ENKSKAVEQVKAFAFKLQ-EKGI 147  
QY 159 VKALGELDILLQWME 173  
DB 148 YKAMSEFDIFINYIE 162

## RESULT 3

146591  
Interleukin 10 - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: 146591  
R:Blanchard, G.; Gianello, P.; Germania, S.; Baetscher, M.; Sachs, D.H.; Leguern, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995  
A:Title: Molecular identification of porcine interleukin 10: regulation of expression in  
A:Reference number: 146591; MUID:95224028; PMID:7708727  
A:Accession: 146591  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-175 <BLA>  
A:Cross-references: UNIPROT:Q29055; GB:L20001; NID:9309792; PIDN:AAA74410.1; PID:9309793  
C:Genetics:  
A:Gene: IL-10  
C:Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 2; Length 175;  
Best Local Similarity 27.0%; Pred. No. 1.1e-07;  
Matches 48; Conservative 34; Mismatches 78; Indels 18; Gaps 6;  
QY 1 MKASLAEFLSAAFFLLMTPTSLKTLNLSGV-----IATNLOEIRNGFSDIRGSVOA 55  
DB 1 MPSSALTYCLT-----FLAGVAASIKSEN--SCIFPTSLPHMLRELRAAGPVKSPQT 53  
QY 56 KDGNDIRLRTESLQDTKPANRCCLRLHLRLYLDRVFNKQTPDHTLRKISLANS 115  
DB 54 KDQMGD-LTLTGLSLEDFKGLGQALSEMIQFYLBVMPKASDGSIDIKHVNLSGEK 111  
QY 116 FLTKKDLRLCHAMTCHGEAMKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173  
DB 112 LKTLRLRLRRCRFLPC---ENKSKAVEQVKAFAFKLQ-EKGIYKAMSEFDIFINYIE 165

## RESULT 4

A48558  
Interleukin 10 homolog - equine herpesvirus 2  
N:Alternate names: hypothetical protein E7  
C:Species: equine herpesvirus 2  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A48558; S55664  
R:Rode, H.J.; Janssen, W.; Rosen-Wolff, A.; Bugert, J.J.; Thein, P.; Becker, Y.; Darat,  
Virus Genes 7, 111-116, 1993  
A:Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 (IL10)-like g  
A:Reference number: A48558; MUID:93227565; PMID:8385838  
A:Accession: A48558  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <ROD>  
A:Cross-references: UNIPROT:Q89451; GB:S59624; NID:9299468; PIDN:AA826148.1; PID:9299469  
A:Note: Sequence extracted from NCBI Backbone (NCBI:129334, NCBI:129335)  
R:Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S55944; MUID:95302501; PMID:7789207  
A:Accession: S55664  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Residues: 1-179 <TEB>  
A:Molecule type: DNA  
A:Cross-references: GB:U20824; NID:9695172; PIDN:AC13857.1; PID:9695242  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995  
C:Superfamily: interleukin-10

Query Match 16.2%; Score 147.5; DB 2; Length 179;  
Best Local Similarity 31.9%; Pred. No. 6e-07;  
Matches 44; Conservative 24; Mismatches 59; Indels 11; Gaps 6;  
QY 39 LOEIRNGFSDIRGSVOAKDGNIDIRLRTESLQDTKPANRCCLRLHLRLYLDRVFNKY 98  
DB 41 LHELRAAFSRVKTFQTKD-QLD-NMLDGLSLEDFKGLGQALSEMIQFYLBVMP-- 96  
QY 99 QTPDHTLR---KISLANSFLTKKDLRLCHAMTCHGEAMKYSQILSHFEKLEPQ 155  
DB 97 QAEHSTQEDKQNSLGEKTLRLRLRRCRFLPC---ENKSKAVEQVKAFAFKLQ-E 152  
QY 156 AAVVKALGELDILLQWME 173  
DB 153 KGVYKAMSEFDIFINYIE 170

## RESULT 5

A34853  
Interleukin-10 precursor - mouse

N: Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10  
C: Species: Mus musculus (house mouse)  
C: Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 09-Jul-2004  
C: Accession: A34853; 156136  
R: Moore, K.W.; Vieira, P.; Fiorentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.  
A: Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr virus  
A: Reference number: A34853; MUID:90273182; PMID:2161559  
A: Accession: A34853  
A: Status: Preliminary  
A: Molecule type: mRNA  
A: Residues: 1-178 <MO>  
A: Cross-references: UNIPROT:P18893; GB:M37897; NID:G198288; PIDN:AAA39274.1; PID:G198288  
R: Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.  
U: Immunol. 140, 3618-3623, 1992  
A: Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and  
A: Reference number: 156136; MUID:92268508; PMID:1350294  
A: Accession: 156136  
A: Status: Preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: DNA  
A: Residues: 1-178 <RES>  
A: Cross-references: GB:M84340; NID:G198291; PIDN:AAA39275.1; PID:G198292  
C: Genetics:  
A: Gene: IL10  
C: Introns: 55/3; 75/3; 126/3; 148/3  
C: Superfamily: Interleukin-10  
C: Keywords: cytokine; lymphokine; T-cell1

Query Match 15.8%; Score 144; DB 2; Length 178;  
Best Local Similarity 31.1%; Pred. No. 1.3e-06;  
Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;

QY 39 LOEIRNGESDIRGVOANDGNIDRIILRTESLQDTKPAKRCCLRLRLYLDRVFNKY 98  
DB 41 LLEIRTAHSQVYKFTQTD-QLD-NILITDSIMQPKCYLCOALSEMIQFTVEWFOA 98  
QY 99 QTPDHYTRKISSLSANSEFTIKDRLCHAHNTCHGSEAMKXSQIISHPEKLEPOAY 158  
DB 99 EKHGPEIKHEHNSLDEKRLTLMRLRCHRFPLC---ENKSAVAVQVNSDFNKLODQ-GV 154  
QY 159 VKALGELDILLQWME 173  
DB 155 YKAMNEFDIFINCIE 169

RESULT 6  
JN0475

Interleukin-10 precursor - rat  
N: Alternate names: cytokine synthesis inhibitory factor  
C: Species: Rattus norvegicus (Norway rat)  
C: Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C: Accession: JN0475; JCI357; S36021  
R: Peng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.  
A: Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and  
A: Reference number: JN0475  
A: Accession: JN0475  
A: Status: nucleic acid sequence not shown  
A: Molecule type: mRNA  
A: Residues: 1-178 <PEN>  
A: Cross-references: UNIPROT:P29456  
R: Goodman, R.E.; Oblak, J.; Bell, R.G.  
A: Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from  
A: Reference number: JCI357; MUID:93080542; PMID:1280414  
A: Accession: JCI357  
A: Molecule type: mRNA  
A: Residues: 1, 'P', -3-64, 'L', 66-178 <GCO>  
A: Cross-references: GB:I02926; NID:G204903; PIDN:AAA1425.1; PID:G204904  
R: Peng, L.  
A: Reference number: S36021  
A: Accession: S36021  
submitted to the EMBL Data Library, July 1991

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-178 <FE2>  
 A:Cross-references: EMBL:X60675; NID:g296620; PIDN:CAA43090.1; PID:g296621  
 C:Superfamily: interleukin-10  
 C:Keywords: cytokine; glycoprotein; lymphokine; T-cell  
 F/1-18/Domain: signal sequence #status predicted <SIG>  
 F/19-178/Product: interleukin-10 #status predicted <MKT>  
 F/29,134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 136; DB 2; Length 178;  
 Best Local Similarity 28.5%; Pred. No. 7.8e-06;  
 Matches 53; Conservative 26; Mismatches 77; Indels 30; Gaps 8;

QY	1	MKASLSLFSLSAFAVLLMTPTSTGLKTLNIGSCVIATN-----LQIRNGPSD	48
DB	1	MLGSLALCCLLILA-----GVKT-SKSHGSRGNNGCTHPVSGTHMLRELRAAFSQ	50
QY	49	IRGSVQAKDGNIDIRILRTES-IQDTKANRCCLRLHLRLYDRVFKNYQTPDHTLR	107
DB	51	VKTFPQKKD-QLDNIIVL--TDSLLQDPKGYGCAALSEMIFYLVEVWPAQENHGPBIKE	107
QY	108	KISLSANFLTIKQDRLCHAHMTCHGGEEMKKYSQILSHFEKLBPQAAVVKALGELDI	167
DB	108	HLNLSIGEKTKTLMTQLRRCHRFPC---ENKSKAVEQKVDENFKLDQK-GYTKAMNEFDI	163
QY	168	LLQWME 173	
DB	164	FINCIE 169	

RESULT 7  
 J05538  
 Rab geranylgeranyl transferase (EC 2.5.1.1) alpha chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: J05538  
 R:Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.  
 Biochem. Biophys. Res. Commun. 235, 10-14, 1997  
 A>Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutamina  
 A:Reference number: J05538; MUID:97339427; PMID:9196026  
 A:Accession: J05538  
 A:Molecule type: DNA  
 A:Residues: 1-567 <SON>  
 A:Cross-references: UNIPROT:Q92696  
 C:Comment: This protein is involved in cutaneous disease. The gene of this enzyme is po  
 C:Genetics:  
 A:Gene: Rabgsta  
 A:Intron: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 413  
 C:Keywords: transferase

Query Match 10.4%; Score 94.5; DB 2; Length 567;  
 Best Local Similarity 25.8%; Pred. No. 0.34;  
 Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;

QY	1	MKASLSLSLSAFAVLLMTPTSTGLKTLNIGSCVIATNLOE--IRNGFSD--IRGSVQA	55
DB	304	LPAAISNDQLPQHTFRVMTAGVOK-----ECVLLKGRQEGMCRDSTTDEGLPRCELSV	358
QY	56	KDGNIDIRILRTESIQDTKANRCCLRLHL-----RLYLDVFKNYQT-----PDH	103
DB	355	ESGYTLQSELSECKQLQELPEPKKCLITLILMLADPLVYKEKTLGYFTLKAVDPMR	418
QY	104	YT---LRKISLSANFLTIK---KDLRLCHAHMTCHGGEEMKKYSQILSH--FEKL	152
DB	419	ATYLDLSEKFLIENSVLKMEYAEVRVHLAKHDKLTVALCHLEQLLLVTHLDSHRLRTL	478
QY	153	EPQAAVVKAL 162	
DB	479	PPALALRCL 488	

RESULT 8

A45977  
Rab geranylgeranyl transferase component B alpha subunit - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45977  
R:Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.  
J. Biol. Chem. 268, 12221-12229, 1993  
J>Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge  
A:Reference number: A45977; MUID:93280201; PMID:8505342  
A:Accession: A45977  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-567 <ARM>  
A:Cross-references: UNIPROT:Q08602; GB:S62096; NID:G385474; PIDN:AA827018.1; PID:G385475  
A:Experimental source: brain  
A>Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBIPI:133370)  
  
Query Match 10.4%; Score 94.5; DB 2; Length 567;  
Best Local Similarity 24.2%; Pred. No. 0.34;  
Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;  
  
Qy 1 MKASLASLSAAYLLMTPTGKLTNLSGCVATNIGF--INGRSD---IRGSVOA 55  
Db 304 LPASLNDQLPQHTFRVMTGSDSK---ECVILKORPECWCSDATDEQLFRCELSTV 358  
Qy 56 KQGNIDIRLRRTESLDPTKPRANRCLRLHLRL-YLDRVFNQYQTPDHYT----- 105  
Db 359 EKSTVLOSELBESCKLOELFENKNCCLITLILMALDPLVYBKETLQYFSLKAVDQMR 418  
Qy 106 -----LRKISSLANSLFTTK---KDLRLCHAHMTCHGSEAMKKYSQI-LSH-FEKL 152  
Db 419 AAYLDLRSKFLKLENSVLMKEYADVRLAHKDLTVLCHLEQLLVTLHLSHRLBAL 478  
Qy 153 EPQAIVKAL 162  
Db 479 PPALALRCL 488  
  
RESULT 9  
S64594  
Probable beta-adaptin YK5 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein G9331; protein YGR261C  
C:Species: Saccharomyces cerevisiae  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004  
R:Armstrong, S.A.; Agostoni Carbone, M.L.; Melchiorreto, P.; Plevani, P.; Martegani, E.; Var  
submitted to the Protein Sequence Database, May 1996  
A:Accession: S64594  
A:Reference number: S64591  
A:Molecule type: DNA  
A:Residues: 1-809 <PAN>  
A:Cross-references: UNIPROT:P46682; EMBL:Z73046; NID:g1323474; PID:e243689; PID:g1323475  
A:Experimental source: strain S288C  
R:Robinson, L.C.; Engle, H.M.; Panek, H.R.  
submitted to the EMBL Data Library, September 1995  
A:Description: Suppressors of loss of yeast casein kinase 1 function define the four sub  
A:Reference number: S63439  
A:Accession: S63450  
A:Molecule type: DNA  
A:Residues: 1-26, 'PLSVNPP', '36-723', 'T', '725-795', 801-809 <ROB>  
A:Cross-references: EMBL:U35411; NID:g1017728; PID:g1017729  
C:Genetics:  
A:Gene: SGD:YK5  
A:Cross-references: SGD:S0003493; MTPS:YGR261C  
A:Map position: 7K  
  
Query Match 10.3%; Score 93.5; DB 2; Length 809;  
Best Local Similarity 24.1%; Pred. No. 0.65;  
Matches 48; Conservative 39; Mismatches 73; Indels 39; Gaps 10;  
  
Qy 2 KASSLASLSAAYLLMTPTGKLTNLSGCVATNIGF--INGRSD---IRGSVOA 61  
Db 21 EAAAVATSKLGESSYTY--SONINPOQLVTLINSNSREVDAMKRITISIMASDDSD 78

Qy 62 IRI-----LRRTESLDPTKPRANRCLRLHLRL-YLDRVFNQYQTPDHYTLRKISSLANSL 117  
Db 79 VQLFPADVKNKITTNDK-----VKRLIHLYLRFEN---DPNLTLSLINSLOKSL 128  
Qy 118 TIKDLRLCHAHMTCHGSEAMKKYSQILSHFEK--LEPOA-----AVTK--ALGE 164  
Db 129 DSNSELR-CFA--LSALSDMGMSSLAPIIHTVTKLVTPSAMVKGVALAIITLYRAGK 185  
Qy 165 -----IDLLOMMEETE 176  
Db 186 NDYHELDIDIKELMADTD 204  
  
RESULT 10  
F83128  
Probable transcription regulator PA4135 (imported) - Pseudomonas aeruginosa (strain PA01  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: F83128  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim,  
Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F83128  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <STO>  
A:Cross-references: UNIPROT:Q9HWP6; GB:AE004830; GB:AE004091; NID:G9950337; PIDN:AA0752  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4135  
  
Query Match 9.3%; Score 85; DB 2; Length 140;  
Best Local Similarity 24.5%; Pred. No. 0.55;  
Matches 25; Conservative 25; Mismatches 42; Indels 10; Gaps 3;  
  
Qy 62 IRIIRRTESLDPTKPRANRCLRLHLRL-YLDRVFNQYQTPDHYTLRKISSLANSL 115  
Db 40 IRIIRQGESESYQLANQACTLRPMGTGLRLERDGVVRMKAKXQOR-RYYVNLTEKG 98  
Qy 116 ---FTIKDLRLCHAHMTCHGSEAMKKYSQILSHFEKLP 154  
Db 99 QQCFTVSGDMKKNYQRIQGRFGEKLAQLLELNLKXIRP 140  
  
RESULT 11  
T3346  
Hypothetical protein C16A11.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T3346  
R:Johnson, D.; Biewald, T.  
submitted to the EMBL Data Library, July 1998  
A:Description: The sequence of C. elegans cosmid C16A11.  
A:Reference number: Z21328  
A:Accession: T3346  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-646 <JOH>  
A:Cross-references: UNIPROT:O76579; EMBL:AF077536; PIDN:AAC26261.1; GSPDB:GN00020; CESP:  
A:Experimental source: strain Bristol N2; clone C16A11  
C:Genetics:  
A:Gene: CESP:C16A11.5  
A:Map position: 2  
A:Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3  
  
Query Match 9.0%; Score 81.5; DB 2; Length 646;  
Best Local Similarity 26.1%; Pred. No. 7.4;  
Matches 36; Conservative 22; Mismatches 49; Indels 31; Gaps 8;

Qy 29 NIGSCVIAITNIOEINGFSDIRGSVOAKDNIDIRL-----RTESLODTTPANRC 80  
 Db 176 NQACAFVBRSLRQ-RNSNDHPIVQELDSMKSIPTIOPRAKKAVIDELKRGSYC 234  
 Qy 81 CL-LHRLRLVLD-----RVEKRYQTPD--HYTLKISLANSPLTIKDLRLCAHMTCC 132  
 Db 235 ILAVALFELFELIIGWSVFEKHVFKIIEYVL-KLPT-----LIFKSELFPFPIKTA 288  
 Qy 133 HCGEEMAKKYSOILSHFE 150  
 Db 289 H-----LHRLLSFE 298

## RESULT 12

S46367  
 protein kinase CDC7 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)  
 CSpecies: Schizosaccharomyces pombe  
 CDate: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 16-Aug-2004  
 CAccession: S46367; T39888  
 R:Fankhauser, C.; Simanis, V.  
 EMBO J. 13, 3011-3019, 1994  
 A>Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in  
 A:Reference number: S46367; PMID:94313982; PMID:8039497  
 A:Accession: S46367  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1062 <FAN>  
 A:Cross-references: UNIPROT:P41892; EMBL:X78799; NID:G521098; PIDN:CAA5382.1; PID:G5210  
 A:Experimental source: wildtype 972 h minus  
 A>Note: mRNA sequencing was also done to confirm the intron borders  
 R:Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, February 1999  
 A:Reference number: Z21860  
 A:Accession: T39888  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-1062 <SAU>  
 A:Cross-references: EMBL:AL035537; PIDN:CA836886.1; GSPDB:GN00067; SPDB:SPBC21.06C  
 A:Experimental source: strain 972h-; cosmid c21  
 C:Genetics:  
 A:Gene: CDC7, SPDB:SPBC21.06C  
 A:Map position: 11; 2  
 A:Insertions: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3  
 C:Function:  
 A:Description: essential for septum formation and cell division  
 C:Superfamily: protein kinase homology  
 C:Keywords: ATP; cell division; phosphotransferase; protein kinase  
 F/7-259/Domain: protein kinase homology <KIN>  
 F/15-23/Region: protein kinase ATP-binding motif

Query Match 8.8%; Score 81; DB 2; Length 1062;  
 Best Local Similarity 30.2%; Pred. No. 15;  
 Matches 32; Conservative 20; Mismatches 44; Indels 10; Gaps 4;  
 Qy 23 TGLKTNLGSQVIAITNIOEIRNG-FSDIRGSVOAKDNIDIRLIRTESLODTTPANRC 81  
 Db 466 TGLCTLVANCKYSGMNNHEDGESDIPDSIERINLENLDIE-----NNTALDKRTILAS 520  
 Qy 82 LLRLRLVLDVRFKRYQTPDHYTLRKISLANSPLTIKDLRLCH 127  
 Db 521 LLSSILGSLRD---KNIGSKD-TTVSQIASILSEDLISLKRRIIOAH 562

## RESULT 13

T19925  
 hypochelical protein C44C10.4 - Caenorhabditis elegans  
 CSpecies: Caenorhabditis elegans  
 CDate: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 CAccession: T19925  
 R:Cottage, A.  
 submitted to the EMBL Data Library, February 1996  
 A:Reference number: Z19197  
 A:Accession: T19925

A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-542 <WIL>  
 A:Cross-references: UNIPROT:Q18616; EMBL:Z69787; PIDN:CAA93638.1; GSPDB:GN00028; CESP:C4  
 A:Experimental source: clone C44C10  
 C:Genetics:  
 A:Gene: CESP:C44C10.4  
 A:Map position: X  
 A:Insertions: 66/3; 229/3; 309/1; 328/3; 398/3

Query Match 8.8%; Score 80; DB 2; Length 542;  
 Best Local Similarity 23.2%; Pred. No. 8.4;  
 Matches 29; Conservative 25; Mismatches 43; Indels 28; Gaps 4;

Qy 39 LOEIRNGSDIRGSVOAKDNIDIRLIRTESLODTTPANRCCLRLRLVLDVRFKRY 98  
 Db 212 IOETKEKVALEQLKVNANAKWPLRISYSBAIPKQTPSPN-----FKQN 256  
 Qy 99 -----QTPDHY-----TLRKISLANSPLTIKDL---RLCAHMTCHCGEEMAKKYQOI 145  
 Db 257 AIVRPKTHNHYDNLITVDKLSYLNKXTERRELLQFAVNHPPNNIRFSEBGRPIVARE 316  
 Qy 146 LSHFE 150  
 Db 317 IDYTE 321

## RESULT 14

AD1160  
 hypochelical protein glp/glnQ (imported) - Agrobacterium tumefaciens (strain C58, Dupon  
 CSpecies: Agrobacterium tumefaciens  
 CDate: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 CAccession: AD1160  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, B.W.  
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:21608550; PMID:11743193  
 A:Accession: AD1160  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-502 <KUR>  
 A:Cross-references: UNIPROT:Q9WMP4; GB:AB008687; PIDN:AAL45698.1; PID:GI7743426; GSPDB:  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: glp/glnQ  
 A:Genome: plasmid

Query Match 8.4%; Score 76.5; DB 2; Length 502;  
 Best Local Similarity 24.6%; Pred. No. 17;  
 Matches 42; Conservative 23; Mismatches 37; Indels 69; Gaps 10;  
 Qy 10 LLSAAYLLMT-PSTGL-----KTLNLSG---CVIATNIOEIRNGSDIRGSVOA----- 55  
 Db 206 LLAGVYLLVTVPLTHVVAIDRLIRIGQRPVSIVTSGLEEV-----SELDGARASGVAR 261  
 Qy 56 KQDNIDIRLIRTESLOD-----TKPANRC-----LLRL----- 86  
 Db 262 KQGSIDVRLGMAVGDLDVAKGVDSVFKPSVTCTIIGPGSGKSTLLRGLNRLVVERKSGD 321  
 Qy 87 -----LRLVLDVRFKRYQTPDHYTLRKISLANSPLTIK 121  
 Db 322 ILIDGESILAMKETLARRVGVFQHPNLFPH-----TALENVWLSLKK 366

## RESULT 15

B90153  
 2-isopropylmalate synthase, probable (leuA-1) (imported) - Sulfolobus solfataricus  
 CSpecies: Sulfolobus solfataricus  
 CDate: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C|Accession: B90153  
R|Shih, Q.; Singh, R.K.; Confalonieri, F.; Ziyanicovic, Y.; Allard, G.; Aways, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.T.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arrett, R.A.; Ragan, M.A.; Senese, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A|Description: *Sulfolobus solfataricus* complete genome.  
A|Reference number: A99139  
A|Accession: B90153  
A|Status: preliminary  
A|Molecule type: DNA  
A|Residues: 1-553 <KUR>  
A|Cross-references: UNIPROT:Q980Z1; GB:AE006641; NID:g13813259; PIDN:AAK40481.1; GSPDB:G-  
C|Gene: leuA-1  
C|Superfamily: 2-Isopropylmalate synthase leuA

Query Match 8.4%; Score 76.5; DB 2; Length 553;  
Best Local Similarity 19.6%; Pred. No. 19;  
Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;

24 GLKTLNLGSCVIAITVLEIRNGFSDIRGSAV-----KQGNID-----IRILRR 67  
232 GIHANNDIGCAVANSIMAIKAGARRHVGQTINGIGERTGNADLIQIPTLLIKMGIANLNG 291  
68 TESIADPTPARCC-----LRLHLRLVLDVRFKRYQTFPH----- 103  
292 QESLKLKEVERIRIYEIILGDPNPYQPYGVNAPRHKAGVHDAVMKVPVRYEHVDPSLV 351  
104 -----YTLRKISLAN--SFL-----TIKDLRLCHAMTCHGGEAMKKYSOILSHFE 150  
352 GNDKRFVISEISGTANLVSYLQGLGIAVDKKDERL-----KRLANKIKELBARGY 401  
151 KLE--PQAAVVKALGELDI 167  
402 SFDVGPASAILITLKEINI 420

Search completed: November 2, 2005, 18:48:01  
Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 2, 2005, 18:40:05 ; Search time 177 Seconds

(without alignments)  
509.186 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 910  
Sequence: 1 MKASSLAFSLISAPFYLIWT.....AVKALGELDILLQMMERTS 176

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	906	99.6	176	1 IL20_HUMAN	Q9NY11 homo sapien
2	672	73.8	176	1 IL20_MOUSE	Q9J1K9 mus musculu
3	337.5	37.1	176	1 IL19_HUMAN	Q9JHD0 homo sapien
4	281.5	30.9	176	2 O8CJ70	Q8CJ70 mus musculu
5	266.5	29.3	175	2 Q7SK60	Q925J3 mus musculu
6	222	24.4	220	2 Q925J3	Q925J3 mus musculu
7	220	24.2	181	2 Q925S4	Q13007 homo sapien
8	217	23.8	206	1 IL24_HUMAN	Q9J124 rattus norv
9	191	21.0	183	1 MOB5_RAT	Q9J124 rattus norv
10	187	20.5	183	2 Q9WYB8	Q9WYB8 rattus norv
11	175.5	19.3	175	2 O6A2H4	O6A2H4 gallus gall
12	175.5	19.3	175	2 O6A2H5	O6A2H5 gallus gall
13	161.5	17.7	178	1 IL10_MACNE	Q8U2J6
14	161	17.7	177	2 Q8U2J6	Q8U2J6 cercopithec
15	157.5	17.3	178	1 IL10_MACFA	P51493 macaca fasc
16	157.5	17.3	178	1 IL10_MACMU	Q7T311 cypripus ca
17	157.5	17.3	180	2 Q7T311	Q7T311 cypripus ca
18	156.5	17.2	150	2 Q7T311	Q7T311 homo sapien
19	156.5	17.2	178	1 IL10_FELCA	P55029 felis silve
20	156.5	17.2	178	1 IL10_HUMAN	P22301 homo sapien
21	155	17.0	170	1 BCRF_EBV	P33180 Epstein-Bar
22	155	17.0	170	2 Q777H2	Q777H2 human herpe
23	155	17.0	175	1 IL10_PIG	Q29055 sus scrofa
24	154.5	17.0	178	1 IL10_CERTO	P46651 cercocebus
25	153	16.8	178	1 IL10_MERUN	P47965 meriones un
26	151.5	16.6	179	1 IL10_CEREL	P51746 cervus elap
27	151	16.6	178	2 Q9T574	Q9T574 cryocolagus
28	147.5	16.2	178	2 Q9TVD3	Q9TVD3 cryocolagus
29	147.5	16.2	178	1 IL10_EH2	Q89451 equine herp
30	147	16.2	179	1 IL10_MOUSE	P18893 mus musculu
31	145.5	16.0	178	2 Q6FGS9	Q6FGS9 homo sapien

## ALIGNMENTS

RESULT 1  
ID IL20\_HUMAN STANDARD; PRT; 176 AA.  
AC Q9NY11; Q9EQ26;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10)  
DB UNQ852/PRO1801).  
GN Name=IL20;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
PI [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21097717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8;  
RA Blumberg H., Conklin D., Xu W.F., Grossman A., Brender T.,  
RA Carollino S., Eagan M., Foster D., Haldeman B.A., Haugen H.,  
RA Jellinek L., Kelly J.D., Madden K., Wagner K., West J.,  
RA Prunkard D., Saxon S., Sprecher C., Waggle K., West J.,  
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.,  
RT "Interleukin 20: discovery, receptor identification, and role in  
RT epidermal function.";  
RT Cell 104:9-19(2001).  
RL [2]  
RP SEQUENCE FROM N.A.  
RX Rieder M.J., Carrington D.P., Chung W.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nicholson D.A.;  
RT "SeattleSNPs: NHLBI HUGO682 program for genomic applications, UW-  
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RT Submitted (JUL-2001) to the EMBL/Genbank/DBD databases.  
RL [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brueh J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,  
RA Vanden R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RT Genome Res. 13:2265-2270(2003).  
RL [4]  
RP SEQUENCE OF 25-39.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";

```

RL Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC peristalsis. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
CC and other tissues.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF224267; AAF36679.1; -.
DR EMBL; AF402002; AAK84423.1; -.
DR EMBL; AY358320; AAO88686.1; -.
DR HSSP; Q9UHD0; INIF.
DR Genem; HGNC:6002; IL20.
DR MIM; 605619; -.
DR GO; GO:0005576; E:extracellular; TAS.
DR GO; GO:0045517; F:interleukin-20 receptor binding; TAS.
DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. . .; TAS.
DR GO; GO:0045618; P:positive regulation of keratinocyte differ. . .; TAS.
DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. . .; TAS.
DR GO; GO:0050727; P:regulation of inflammatory response; TAS.
DR InterPro; IPR000098; Interleukin_10.
DR Prodom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR KW Cytokine; Direct protein sequencing; Signal.
FT CHAIN 1 24 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
FT CONFLICT 48 48 E -> D (in Ref. 1).
FT CONFLICT 126 126 C -> S (in Ref. 3).
SQ SEQUENCE 176 AA; 20072 MW; 8385992500B6C447 CRC64;

Query Match 99.6%; Score 906; DB 1; Length 176;
Best Local Similarity 99.4%; Pred. No. 1.3e-80;
Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLASLSAAYFLMTPTSTGLKTNLGSQVATNLQETIRNGFSIRDSVOAKDNI 60
DB 1 MKASSLASLSAAYFLMTPTSTGLKTNLGSQVATNLQETIRNGFSIRDSVOAKDNI 60
QY 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
DB 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
QY 121 KDLRLCHAMTCHGGEEMAKKYSQILSHPEKLEPQAAVYKALGELDILLQNMEE 176
DB 121 KDLRLCHAMTCHGGEEMAKKYSQILSHPEKLEPQAAVYKALGELDILLQNMEE 176

RESULT 2
IL20_MOUSE STANDARD; PRT; 176 AA.
ID IL20_MOUSE
AC Q9JUV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).
GN Name=IL20;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Skin;
RX MEDLINE=21097717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg P., Conklin D., Xu W.F., Grossman A., Bender T.,
RA Carrollo S., Sagen M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggle K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.,
RA Interleukin 20: discovery, receptor identification, and role in
RA epidermal function.*;
RL Cell 104:9-19(2001).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC peristalsis. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AF224267; AAF36680.1; -.
DR HSSP; Q9UHD0; INIF.
DR MGD; MGI:1890473; IL20.
DR GO; GO:0045517; F:interleukin-20 receptor binding; IPI.
DR InterPro; IPR000079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR Prodom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR KW Cytokine; Signal.
FT CHAIN 1 24 Potential.
FT DISULFID 25 176 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
SQ SEQUENCE 176 AA; 20097 MW; 08577AF656574771 CRC64;

Query Match 73.8%; Score 672; DB 1; Length 176;
Best Local Similarity 75.3%; Pred. No. 1.1e-57;
Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKASSLASLSAAYFLMTPTSTGLKTNLGSQVATNLQETIRNGFSIRDSVOAKDNI 60
DB 1 MKGFGLAFLGSAVGFLLMTPLTGKTHLALSSCVITANLQAIQKFSIRDSVOAKDNI 60
QY 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
DB 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
QY 121 KDLRLCHAMTCHGGEEMAKKYSQILSHPEKLEPQAAVYKALGELDILLQNMEE 174
DB 121 KDLVCHSHMAHCHGGEEMAKKYNQILSHFIELQPAVYKALGELGILLRWME 174

RESULT 3
IL19_HUMAN STANDARD; PRT; 177 AA.
ID IL19_HUMAN
AC Q9UHD0; Q96OR4; Q9NUA0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Interleukin-19 precursor (NG.1).
DE protein-like protein (NG.1).
GN Name=IL19; Synonyms=zMDA1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RX MEDLINE=21040165; PubMed=11196675; DOI=10.1038/sj.gene.6363714;  
RA Gallagher G., Dickensheets H., Eskdale J., Izotova L.S.,  
RA Mitrochitschenko O.V., Peat J.D., Vasquez N., Pestka S., Donnelly R.P.,  
RA Korten S.V.,  
RT "Cloning, expression and initial characterization of interleukin-19  
RT (IL-19), a novel homolog of human interleukin-10 (IL-10).",  
RT Genes Immun. 1:442-450(2000).  
RL (1)  
RP SEQUENCE FROM N.A.  
RA Conlin D., Petersen J., Loften-Day C., Whitmore T., Muerer M.,  
RA Sexson S., Smith D., Lok S., Pomeroy T., O'Hara P.,  
RT "Human sapiens homolog of melanoma differentiation associated gene";  
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN (3)  
RP SEQUENCE FROM N.A.  
RA Korten S.V., Pestka S.,  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN (4)  
RP SEQUENCE FROM N.A., AND VARIANT PHE-175.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.,  
RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UM-  
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN (5)  
RP SEQUENCE OF 98-177 FROM N.A.  
RA Hall R.,  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN (6)  
RP SEQUENCE OF 25-39.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.,  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RT Protein Sci. 13:2819-2824(2004).  
RL (1)  
RP SUBCELLULAR LOCATION: Secreted.  
CC (1)  
CC (1) SIMILARITY: Belongs to the IL-10 family.  
CC -----  
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CC or send an email to [license@sib-ch.ch](mailto:license@sib-ch.ch)).  
CC -----  
DR EMBL; AF276915; AAC16755.1; -  
DR EMBL; AF192498; AAF06663.1; -  
DR EMBL; AY040367; AAK91776.1; ALT\_INIT.  
DR EMBL; AF390905; AAK64498.1; -  
DR EMBL; AL049615; CAB72342.1; -  
DR PDB; 1NIF; X-ray; A=19-177.  
DR Genew; HGNC:5990; IL19.  
DR MIM; 605687; -  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005125; F:Cytokine activity; TAS.  
DR GO; GO:0006955; P:Immune response; NAS.  
DR GO; GO:0007165; P:signal transduction; NAS.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000098; Interleukin\_10.  
DR SMART; SM00188; IL10; 1.  
DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
KW 3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;  
KW Polymorphism; Signal.  
FT SIGNAL 24  
FT CHAIN 1  
FT CARBOHYD 25 177 Interleukin-19.  
FT CARBOHYD 56 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 135 N-linked (GlcNAc...) (Potential).  
FT VARIANT 175 S->F.  
FT SEQUENCE 177 AA; 20392 MW; 7CCFAC22177DE408 CRC64;  
SQ  
Query Match 37.1%; Score 337.5; DB 1; Length 177;

Best Local Similarity 39.7%; Pred. No. 6,7e-25;  
Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;  
QY 1 MKASLAIFSLAFAFYLLMTPTSGTKTLNLSGCVATNIOEIRNGFSIDRGVQAKDGN 60  
DB 1 MKQCVSLMLGTLITLCSVDNHGR-----RLISTDMHHEESFOEIKRAIOAADTTP 55  
QY 61 DIRLRRTRESLODTPPARCCLLRLRLYLDRVRKNVOTPPHYTLRKISLANSPLYTK 120  
DB 56 NYTILSTLETDQIIPKPDVCCVTKNLAPYDVRFVDHQPMPKILRKISLANSPLYNQ 115  
QY 121 KDLRLCHAMTCHGCEAMKKYSQILSHPEKLEPQAAVVKALGELDILQNMEE 174  
DB 116 KTLRQCEORQCHCRQEAATNATRVVHDNYDQLEVMAAIAKSLGELDVFLAMLNK 169

RESULT 4  
ID 08CJ70 PRELIMINARY; PRT; 176 AA.  
AC 08CJ70;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Interleukin 19 (Fragment).  
GN Name=IL19;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss Webster/NIH;  
RX MEDLINE=22257669; PubMed=12370360;  
RA Liao Y.C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.S.;  
RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell  
RT apoptosis through TNF-alpha";  
RT J. Immunol. 169:4288-4297(2002).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss Webster/NIH;  
RA Liao Y.-C., Chang M.-S.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF453945; AAN40905.1; -  
DR HSSP; Q9UHD0; 1NIF.  
DR MGD; MGI:1890472; IL19.  
DR GO; GO:0006917; P:induction of apoptosis; IDA.  
DR GO; GO:0042326; P:interleukin-6 biosynthesis; IDA.  
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000098; Interleukin\_10.  
DR PRODOM; PD003687; Interleukin\_10; 1.  
DR SMART; SM00188; IL10; 1.  
FT NON TER 1  
FT SEQUENCE 176 AA; 20287 MW; 73B6C1BC5407FDC CRC64;  
SQ  
Query Match 30.3%; Score 281.5; DB 2; Length 176;  
Best Local Similarity 38.6%; Pred. No. 2.1e-19;  
Matches 56; Conservative 35; Mismatches 53; Indels 1; Gaps 1;  
QY 29 NLGSCVATNLOIRNGFSIDRGVQAKDGNIRIRLRRTRESLODTPPARCCLLRLRL 88  
DB 24 SLRCLISVIMRLKESFHKRAMQTKDTPKNTVL-SLENLRISRGVCCNTNNLLT 82  
QY 89 LYLDRVFNKVTQTPDHYTLRKISLANSFLTIKDLRLCHAMTCHGCEAMKKYSQILSH 148  
DB 83 FYNDRVQDQHQBSESLVLRRISSIANSLFCVQSLKRCYVHRQNCGSEATNATRIHDN 142  
QY 149 FEKLEPQAAVVKALGELDILQNMEE 173  
DB 143 YNQLVSSAALKSLGELNILLAMWD 167  
RESULT 5

Q7SK60  
ID Q7SK60 PRELIMINARY; PRT; 175 AA.  
AC Q7SK60;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Interleukin-20.  
GN Name=IL20;  
OS Tetradon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetradon.  
OX NCBI\_TaxId=99883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12869211; DOI=10.1186/1471-2164-4-29;  
RA Lutfalla G., Crolius H.R., Stange-Thomann N., Jallion O.,  
Mogensen K., Monneron D.;  
RT "Comparative genomic analysis reveals independent expansion of a  
RT lineage-specific gene family in vertebrates: the class II cytokine  
RT receptors and their ligands in mammals and fish."  
RL BMC Genomics 4:29-29(2003).  
DR EMBL; AY29457; AAP57414.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005576; C:cytokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000098; Interleukin\_10.  
DR ProDom; PD003687; Interleukin\_10.  
DR SMART; SMO0188; IL10; 1.  
SQ SEQUENCE 175 AA; 19838 MW; D86FA67E0038E034 CRC64;

Query Match 29.3%; Score 266.5; DB 2; Length 175;  
Best Local Similarity 38.0%; Pred. No. 66-18;  
Matches 57; Conservative 33; Mismatches 53; Indels 7; Gaps 3;

QY 26 KTLNKGSCYATATNLQIRNGFSDIRGSGVQAKGNDIRLRTSLQTPKRNCCLRH 85  
DB 24 QTLVDSGCSISADLQMHQHSNINLNAITTEDEIGVKLSK-RIMEDVQDQRCCTRL 82  
QY 86 LRLYLVDYFVKYQTPDHYTLARKISLSANSPLTI--KQDLRLCHAMTCHCGEAMKYS 143  
DB 83 VLQFIDYKFPYLSHPNQSSSLANTFIIYRKQKIQCH----CLGGEYQKVD 138  
QY 144 QILSHPEKLEPOAAVYKALGELDILLQWME 173  
DB 139 SLIDAFNKLKASKAVLKAVGELDTVLQWLO 168

RESULT 6  
ID Q925J3 PRELIMINARY; PRT; 220 AA.  
AC Q925J3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Th2-specific cytokine FISP.  
GN Name=IL24;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BALB/c;  
RX MEDLINE=21240641; PubMed=11342597;  
RA Schaefer G., Venkataraman C., Schindler U.,  
RT "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule  
RT secreted by Th2 cells."  
RL J. Immunol. 166:5859-5863(2001).  
DR EMBL; AF333251; AAK52470.1; -;

DR MGD; MGI:2135548; IL24.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR ProDom; PD003687; Interleukin\_10; 1.  
DR SMART; SMO0188; IL10; 1.  
DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
SQ SEQUENCE 220 AA; 25168 MW; 5BF76C8612AC909D CRC64;

Query Match 24.4%; Score 222; DB 2; Length 220;  
Best Local Similarity 34.4%; Pred. No. 1.86-13;  
Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LLMTPSTGL--KTINLQSC-VIATNLQIRNGFSDIRGSGVQAKGNDIRLRTSLQD 73  
DB 55 LLMNQVPLBQGFRRFSGCYGTGVLPDLMAFWTKVQTQDDITSIRLL-KQVLRN 113  
QY 74 TKPANRCLLHLRLVLDYRFPKYQT--PDHYTLARKISLSANSPLTIKQDLRLCHAMT 131  
DB 114 VSGASCYLAHSLKFTYNTVFKYHSKIAKFKYLRSTLANNFIVIMSQLQPSKNSM 173  
QY 132 CHCGEAMKYSQILSHPEKLEPOAAVYKALGELDILLQWME 174  
DB 174 LPISBSAQRFLLPRAFKQDTEVALYKAGGEVDILLTMQK 216

RESULT 7  
ID Q925S4 PRELIMINARY; PRT; 181 AA.  
AC Q925S4;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Melanoma differentiation associated gene-7.  
GN Name=IL24;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SvJ;  
RA Madiredi M.T., Lin J., Su Z., Shay J.W., Huberman E., Fisher P.B.;  
RL Submitted (FBI-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF235006; AAK52590.1; -;  
DR MGD; MGI:2135548; IL24.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR ProDom; PD003687; Interleukin\_10; 1.  
DR SMART; SMO0188; IL10; 1.  
DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
SQ SEQUENCE 181 AA; 20812 MW; 05CA43872D53D555 CRC64;

Query Match 24.2%; Score 220; DB 2; Length 181;  
Best Local Similarity 34.4%; Pred. No. 2.36-13;  
Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LLMTPSTGL--KTINLQSC-VIATNLQIRNGFSDIRGSGVQAKGNDIRLRTSLQD 73  
DB 16 LLMNQVPLBQGFRRFSGCYGTGVLPDLMAFWTKVQTQDDITSIRLL-KQVLRN 74  
QY 74 TKPANRCLLHLRLVLDYRFPKYQT--PDHYTLARKISLSANSPLTIKQDLRLCHAMT 131  
DB 75 VSGASCYLAHSLKFTYNTVFKYHSKIAKFKYLRSTLANNFIVIMSQLQPSKNSM 134  
QY 132 CHCGEAMKYSQILSHPEKLEPOAAVYKALGELDILLQWME 174  
DB 135 LPISBSAQRFLLPRAFKQDTEVALYKAGGEVDILLTMQK 177

RESULT 8  
ID IL24\_HUMAN STANDARD; PRT; 206 AA.  
AC Q13007; Q96D80; Q96KG4;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)



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DT 28-FEB-2003 (Rel. 41, last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
DE Cytokine-like protein Mob-5 precursor.
GN Name=Mob5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RA Zhang R., Tan Z., Liang P.;
RT "Identification of a novel ligand-receptor pair constitutively
RL J. Biol. Chem. 275:24436-24443(2000).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
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DR EMBL; AF269251; AAF7553.1; -.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 183 Cytokine-like protein Mob-5.
FT CAROXYD 76 76 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 183 AA; 21096 MW; AF7A11466C491AC4 CRC64;

Query Match
Best Local Similarity 33.1%; Score 191; DB 1; Length 183;
Matches 49; Conservative 31; Mismatches 60; Indels 8; Gaps 5;

QY 31 GSC-VIATNLQIRNGFSDIRGSVQAKDGNIDIRLRTSLODTKPNRCCLLRHLLRL 89
DB 34 GPCQVTGVLPBELWEAFVTKVTKVQDELTSVRL-KPQVLQVSDAESCYLAHSLIKF 92
QY 90 YLDKVFKNYQTP--DHYTLRKISLSLANSFLTIKKDLRLCHAMTCHGSEAMKXYSQILS 147
DB 93 YLNTVFKNYHSKIVKFKYKLSFSTLANNFLVMSKLOPSKONAMLPISDSARRRFLLY 150
QY 148 H--PEKLEPOAAVVKALGELDILQWME 173
DB 151 HRTFKQLDIEVALAKAFGEVDILAMWQ 178

RESULT 10
Q9WVP8 PRELIMINARY; PRT; 183 AA.
AC Q9WVP8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=99308886; PubMed=10381256;
RX DOI=10.1002/(SICI)1097-4644(19990701)74:1<1::AID-UCBJ3-3.3.CO;2-D;
RX Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,

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RA Chiu R., Tieu A., Ting K.;
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7.";
RL J. Cell. Biochem. 74:1-10(1999).
DR EMBL; AF004774; AAB69171.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 183 AA; 21052 MW; FF69A96AFC473E4F CRC64;

Query Match
Best Local Similarity 32.2%; Score 187; DB 2; Length 183;
Matches 47; Conservative 29; Mismatches 66; Indels 4; Gaps 3;

QY 31 GSC-VIATNLQIRNGFSDIRGSVQAKDGNIDIRLRTSLODTKPNRCCLLRHLLRL 89
DB 34 GPCQVTGVLPBELWEAFVTKVTKVQDELTSVRL-KPQVLQVSDAESCYLAHSLIKF 92
QY 90 YLDKVFKNYQTP--DHYTLRKISLSLANSFLTIKKDLRLCHAMTCHGSEAMKXYSQILS 147
DB 93 YLNTVFKNYHSKIVKFKYKLSFSTLANNFLVMSKLOPSKONAMLPISDSARRRFLFHR 152
QY 148 HPEKLEPOAAVVKALGELDILQWME 173
DB 153 TFKQLDIEVALAKAFGEVDILAMWQ 178

RESULT 11
Q6A2H4 PRELIMINARY; PRT; 175 AA.
AC Q6A2H4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rotwell L., Young J., Zoorob R., Whitaker C.A., Hesketh P.,
RA Archer A., Smith A.L., Kaiser P.;
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Blumeria maxima.";
RL J. Immunol. 173:2675-2682(2004).
DR EMBL; AJ621614; CAP21727.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20496 MW; A4966ABAADF8057 CRC64;

Query Match
Best Local Similarity 30.3%; Score 175.5; DB 2; Length 175;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASLAFSLAAYLWMTSTGKLTNLG-SCVIATNLQIRNGFSDIRGSVQAKDGN 59
DB 1 MTCQALLLLLAATL--PAHCLPCTCLFSLIPRLRLKRFKFEIKDYFSRDE 57
QY 60 IDIRLRTESLODTKPNRCCLLRHLLRLYLDKVFKNYQTPDHYTLRKISLSLANSFLTI 119

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Db      58 LNIQIL-SELLDEFGTFCQSVSEMLFYTDEVLPRAMQSTSHQSGMDLGNMLLGL 116
      120 KQDLRLCHAMTCHGCEAMKRYQSILSHFEKLEPQAAVVKALGELDILLOMMEE 174
      117 KATIRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIVKAMGBDIFINYIEE 167

```

## RESULT 12

```

ID      06A2H5      PRELIMINARY;      PRT;      175 AA.
AC      06A2H5;
DT      25-OCT-2004 (TREMBLrel. 28, Created)
DT      25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE      Interleukin-10.
GN      Name=IL-10;
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]

```

```

RP      SEQUENCE FROM N.A.
RA      Rotmwell L., Young J., Zorob R., Whitaker C.A., Heskech P.,
RT      "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT      Immune Response to Elmeria maxima."
RL      J. Immunol. 173:2675-2682 (2004).
DR      EMBL; AF621254; CAP18432.1; -.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0005125; P:cytokine activity; IEA.
DR      GO; GO:0006955; P:immune response; IEA.
DR      InterPro: IPR009079; 4 helix cytokine.
DR      InterPro: IPR000098; Interleukin_10.
DR      Pfam; PF00726; IL10; 1.
DR      PRINTS; PR01294; INTERLEUKIN10.
DR      ProDom; PD003687; Interleukin_10; 1.
DR      SMART; SM00188; IL10; 1.
SQ      SEQUENCE 175 AA; 20514 MW; B0966BEAFB050 CRC64;

```

```

Query Match      19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 5e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

```

```

QY      1 MKASSLAFSLISAFLIWTSPGKLTNG-SCVIAIWNQIRNGPSDIRGSVOADGN 59
      1 MPTCCQALLLILACTL---PAHCLEPTCLHSELPLRLRLKLVKFEIKDYFQSRHDE 57
      60 IDIRIRRTESLDOTKPRANRCLRLRLYLDRVFKNYOTPPHYTLRKISSIANSEFLT 119
      58 LNIQIL-SELLDEFGTFCQSVSEMLFYTDEVLPRAMQSTSHQSGMDLGNMLLGL 116
      120 KQDLRLCHAMTCHGCEAMKRYQSILSHFEKLEPQAAVVKALGELDILLOMMEE 174
      117 KATIRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIVKAMGBDIFINYIEE 167

```

## RESULT 13

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ID      IL10_MACNE      STANDARD;      PRT;      178 AA.
AC      P51497;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory
DE      factor) (CSIF).
GN      Name=IL10;
OS      Macaca nemestrina (Pig-tailed macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9545;

```

```

      22 STGLKTLNIGSCV-----IATNLOIRNGPSDIRGSVOADGNIDIRIRRTESLDOTK 76
      19 SPQGTQSENSCTRFPGNPLPHMLRDADAFSRVTFQKMD-OLD-NILKESLDEFPKG 76
      77 ANRCCILRLRLYLDRVFKNYOTPPHYTLRKISSIANSEFLTIKQDLRLCHAMTCHG 136
      77 YLGGQALSEMIQYLYBVMVQAEHNDPDIKEHVNISGEMIKTURLRLRCHRFPLPC---E 133
      137 EAMKRYQSILSHFEKLEPQAAVVKALGELDILLOMMEE 173
      134 NKSRAVEQWNAFSPKQ-EKGVYKAMSEDFIFINYIEE 169

```

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=PT 10000;
RX      MEDLINE=96003435; PubMed=7561102;
RA      Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT      "Comparative sequence analysis of cytokine genes from human and
RT      nonhuman primates."
RL      J. Immunol. 155:3946-3954 (1995).

```

```

CC      -1- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC      including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC      activated macrophages and by helper T cells (By similarity).
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Belongs to the IL-10 family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).

```

```

DR      HSBP; L26031; AAA9976.1; -.
DR      HSBP; P22301; ILK3.
DR      GO; GO:0005576; C:extracellular; ISS.
DR      GO; GO:0005141; P:interleukin-10 receptor binding; ISS.
DR      GO; GO:0006916; P:anti-apoptosis; ISS.
DR      GO; GO:0030183; P:B-cell differentiation; ISS.
DR      GO; GO:0042100; P:B-cell proliferation; ISS.
DR      GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR      GO; GO:0030097; P:hemopoiesis; ISS.
DR      GO; GO:0006954; P:inflammatory response; ISS.
DR      GO; GO:0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR      GO; GO:0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR      GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR      GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
DR      GO; GO:0045191; P:regulation of isotype switching; ISS.
DR      GO; GO:0042092; P:T-helper 2 type immune response; ISS.
DR      GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR      InterPro: IPR009079; 4 helix cytokine.
DR      InterPro: IPR000098; Interleukin_10.
DR      Pfam; PF00726; IL10; 1.
DR      PRINTS; PR01294; INTERLEUKIN10.
DR      ProDom; PD003687; Interleukin_10; 1.
DR      SMART; SM00188; IL10; 1.
DR      PROSITE; PS00520; INTERLEUKIN_10; 1.
FT      CYTOKINE; Glycoprotein; Signal.
FT      SIGNAL; 1 18
FT      CHAIN; 19 178
FT      DISULFID; 30 126
FT      DISULFID; 80 132
FT      CARBOHYD; 134 134
SQ      SEQUENCE 178 AA; 20560 MW; 35CC0D9D49E70718 CRC64;

```

```

Query Match      17.7%; Score 161.5; DB 1; Length 178;
Best Local Similarity 28.7%; Pred. No. 1.2e-07;
Matches 45; Conservative 31; Mismatches 70; Indels 11; Gaps 5;

```

```

QY      22 STGLKTLNIGSCV-----IATNLOIRNGPSDIRGSVOADGNIDIRIRRTESLDOTK 76
      19 SPQGTQSENSCTRFPGNPLPHMLRDADAFSRVTFQKMD-OLD-NILKESLDEFPKG 76
      77 ANRCCILRLRLYLDRVFKNYOTPPHYTLRKISSIANSEFLTIKQDLRLCHAMTCHG 136
      77 YLGGQALSEMIQYLYBVMVQAEHNDPDIKEHVNISGEMIKTURLRLRCHRFPLPC---E 133
      137 EAMKRYQSILSHFEKLEPQAAVVKALGELDILLOMMEE 173
      134 NKSRAVEQWNAFSPKQ-EKGVYKAMSEDFIFINYIEE 169

```

## RESULT 14





FT	DISULEFD	80	132	By similarity.
FT	CARBOHYD	134	134	N-linked (GlcNAc... ) (Potential)..
SQ	SEQUENCE	178 AA;	20585 MW;	35CEDD98B3B8A718 CRC64;

Query Match	17.3%	Score 157.5	DB 1	Length 178
Best Local Similarity	28.7%	Pred. No. 2.9e-07		
Matches 45, Conservative	30, Mismatches 71,			Indels 11, Gaps 5,

Matches 45; Conservative 30; Mismatches 71; Indels 11; Gaps 5;

Query Match	Score	DB 1	Length
17.34	157.5	178	

Matches 45; Conservative 30; Mismatches 71; Indels 11; Gaps 5;

Matches 45; Conservative 30; Mismatches 71; Indels 11; Gaps 5;

22 STGLKTLNLGCV-----IATNLQEI RNGFS DIRGSVQAKDGNIDIRILRRTESLQDTKP 76

Db 19 SPGGTGSNSCTRPGNLPHMLRDLDAFSRVKTFQMKD-QLD-NILLKESLLEDFKG 76

77 ANRCCLLRHLLRYLDRVFNQYQTPDHYTLRKISSLSANSFLTICKDLRLCHAHMTCHGE 136

Db 77 YLGCQALSEMIQFYLEEVMPPQAENHDPDIKEHVNSLGENLKTLLRLRLRCHRELP---E 133

137 EAMIKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173

Db 134 NKSKEQVKNFSLQ-EKGVKAMSEFDIFINYLE 169

Search completed: November 2, 2005, 18:51:05

Job time : 180 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2005, 18:48:07 ; Search time 176 Seconds  
(without alignments)  
512.079 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 176  
Sequence: 1 MKASSLAPSLSAFYLLMT.....AVVKALGDLIDLLQMEETR 176

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4229

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	128	72.7	176	1	IL20_HUMAN	Q9NYI1 homo sapien
2	13	7.4	176	1	IL20_MOUSE	Q9JXV9 mus musculi
3	8	4.5	137	2	IL2K4	O612K4 picophilus
4	8	4.5	249	1	SURE_PSPPK	O88M11 pseudomonas
5	8	4.5	279	2	O9KDB7	O9KDB7 bacillus ha
6	8	4.5	305	2	O8UIB8	O8UIB8 agrobacteri
7	8	4.5	396	2	O82S35	O82S35 nitrosomona
8	8	4.5	489	1	ANSP_STRCO	O9X7P0 streptomyce
9	8	4.5	517	1	MURE_BIFLO	O894M3 bifidobacte
10	8	4.5	531	2	O7ZVGO	O7ZVGO brachybanio
11	8	4.5	698	2	O83BA7	O83BA7 coxiella bu
12	8	4.5	717	1	P5CS_LYCES	Q964E0 l. delta 1-p
13	8	4.5	719	2	O7MBR3	Q7MBR3 vibrio vuln
14	8	4.5	762	2	O8E874	O8E874 shewanella
15	8	4.5	762	2	O9XGC4	O9XGC4 vitis vinif
16	8	4.5	1277	2	O6SLB3	O6SLB3 cochlidiolu
17	8	4.5	1908	2	O8ASB3	O8ASB3 bacteroides
18	8	4.0	69	2	O8ITP9	O8ITP9 methanosarc
19	8	4.0	90	2	O8NTP1	O8NTP1 corynebacte
20	8	4.0	91	2	O8UUS4	O8UUS4 gallus galli
21	8	4.0	94	2	O8UUG7	O8UUG7 gallus galli
22	8	4.0	96	2	O8CES3	O8CES3 mus musculi
23	8	4.0	97	2	O76Z23	O76Z23 bacterioph
24	8	4.0	97	2	O8R9M3	O8R9M3 thermosane
25	8	4.0	98	2	O6ITW6	O6ITW6 cordylus wa
26	8	4.0	107	2	O846H4	O846H4 uncultured
27	8	4.0	122	2	O6MAG4	O6MAG4 paracitlamed
28	8	4.0	122	2	O6IUM3	O6IUM3 human immun
29	8	4.0	125	2	O7RWX0	O7RWX0 neurospora
30	8	4.0	131	2	O9RLP5	O9RLP5 planktochri
31	8	4.0	138	2	O9K4X8	O9K4X8 planktochri

32	7	4.0	141	2	O8MPC9	O8MPC9 taenia soli
33	7	4.0	145	2	O8B188	O8B188 san miguel
34	7	4.0	152	2	O74J72	O74J72 lactobacill
35	7	4.0	156	2	O6TV02	O6TV02 yaba monkey
36	7	4.0	167	2	O8GBW7	O8GBW7 planktochri
37	7	4.0	172	2	O9R385	O9R385 planktochri
38	7	4.0	172	2	O9RLP3	O9RLP3 planktochri
39	7	4.0	172	2	O9RLP6	O9RLP6 planktochri
40	7	4.0	183	2	O6SXE9	O6SXE9 oryza sativ
41	7	4.0	184	2	O6B0Y9	O6B0Y9 arabidopsis
42	7	4.0	194	2	O6DC06	O6DC06 brachydanio
43	7	4.0	195	2	O9DB50	O9DB50 lotus japon
44	7	4.0	196	1	RAC2_LOTJA	O6V0U7 xanthomonas
45	7	4.0	197	2	O6V0U7	O6V0U7 streptomyce
46	7	4.0	201	2	O07640	O07640 caenorhabdi
47	7	4.0	208	2	O17158	O17158 caenorhabdi
48	7	4.0	210	2	O9K4W9	O9K4W9 oscillator
49	7	4.0	213	2	O9S1Y7	O9S1Y7 arabidopsis
50	7	4.0	217	2	O91ZY6	O91ZY6 rattus norv
51	7	4.0	217	2	O35047	O35047 mus musculi
52	7	4.0	218	2	O6S109	O6S109 paenibacill
53	7	4.0	224	1	G1DB_MYCTU	O53597 mycobacteri
54	7	4.0	235	2	O6H5U4	O6H5U4 oryza sativ
55	7	4.0	236	2	O6DVL7	O6DVL7 thermobia d
56	7	4.0	236	2	O9K4X7	O9K4X7 planktochri
57	7	4.0	240	2	O8GBV7	O8GBV7 oscillator
58	7	4.0	241	2	O9RSX2	O9RSX2 deinococcus
59	7	4.0	242	2	O6S1M0	O6S1M0 burkholderi
60	7	4.0	242	2	O6S1M3	O6S1M3 burkholderi
61	7	4.0	244	2	O9T1X9	O9T1X9 cyanididum c
62	7	4.0	244	2	O882J9	O882J9 pseudomonas
63	7	4.0	245	2	O9K4X2	O9K4X2 oscillator
64	7	4.0	245	2	O9K4X4	O9K4X4 caenorhabdi
65	7	4.0	251	2	O22186	O22186 caenorhabdi
66	7	4.0	262	2	O6DVL4	O6DVL4 thermobia d
67	7	4.0	263	2	O71U37	O71U37 gallus galli
68	7	4.0	282	2	O7U7E8	O7U7E8 synecococc
69	7	4.0	285	2	O6DJP2	O6DJP2 xenopus lae
70	7	4.0	289	2	O8KXA7	O8KXA7 chlorobium
71	7	4.0	289	2	O92QW7	O92QW7 rhizobium m
72	7	4.0	291	2	O8TRQ7	O8TRQ7 methanosarc
73	7	4.0	293	2	O9ZCP1	O9ZCP1 rickettsia
74	7	4.0	298	2	O8B3A4	O8B3A4 pseudomonas
75	7	4.0	304	2	O8ITL0	O8ITL0 arabisidopsis
76	7	4.0	308	2	O94A06	O94A06 xenopus tto
77	7	4.0	308	2	O6DVA5	O6DVA5 vibrio para
78	7	4.0	310	2	O87KJ6	O87KJ6 xenopus lae
79	7	4.0	318	2	O6GLN0	O6GLN0 xenopus lae
80	7	4.0	321	2	O81V85	O81V85 bacillus an
81	7	4.0	321	2	O8B1C8	O8B1C8 pseudomonas
82	7	4.0	327	2	O67164	O67164 aquilex aeo
83	7	4.0	328	2	O83BM7	O83BM7 coxiella bu
84	7	4.0	332	2	O8P2B7	O8P2B7 streptococc
85	7	4.0	333	2	O6GMH6	O6GMH6 lycopersico
86	7	4.0	335	2	O6CTU9	O6CTU9 kluyveromyc
87	7	4.0	344	2	O6CTU9	O6CTU9 kluyveromyc
88	7	4.0	345	2	O9A1A0	O9A1A0 streptococc
89	7	4.0	346	2	O38943	O38943 arabisidopsis
90	7	4.0	354	2	O04440	O04440 arabisidopsis
91	7	4.0	367	2	O751E0	O751E0 oryza sativ
92	7	4.0	368	2	O8U2K8	O8U2K8 pyrococcus
93	7	4.0	382	2	O37395	O37395 allomyces m
94	7	4.0	389	1	GALI_LACHE	O00052 lactobacill
95	7	4.0	389	1	EP1G_DNUCA	O39688 daucus caro
96	7	4.0	391	2	O74K34	O74K34 lactobacill
97	7	4.0	391	2	O81CD6	O81CD6 bacillibacill
98	7	4.0	394	2	O6NCT8	O6NCT8 rhodospseudo
99	7	4.0	398	2	O6XOG9	O6XOG9 sus scrofa
100	7	4.0	411	2	O9BT50	O9BT50 homo sapien
101	7	4.0	413	2	O8EPQ2	O8EPQ2 shewanella
102	7	4.0	414	2	O6BZX3	O6BZX3 yarrowia li
103	7	4.0	419	2	O72Q94	O72Q94 leptospira
104	7	4.0	423	2	O72NS0	O72NS0 leptospira

O8MPC9 taenia soli  
O8B188 san miguel  
O74J72 lactobacill  
O6TV02 yaba monkey  
O8GBW7 planktochri  
O9R385 planktochri  
O9RLP3 planktochri  
O9RLP6 planktochri  
O6SXE9 oryza sativ  
O6B0Y9 arabidopsis  
O6DC06 brachydanio  
O9DB50 lotus japon  
O6V0U7 xanthomonas  
O07640 streptomyce  
O17158 caenorhabdi  
O9K4W9 oscillator  
O9S1Y7 arabidopsis  
O91ZY6 rattus norv  
O35047 mus musculi  
O6S109 paenibacill  
O53597 mycobacteri  
O6H5U4 oryza sativ  
O6DVL7 thermobia d  
O9K4X7 planktochri  
O8GBV7 oscillator  
O9RSX2 deinococcus  
O6S1M0 burkholderi  
O6S1M3 burkholderi  
O9T1X9 cyanididum c  
O882J9 pseudomonas  
O9K4X2 oscillator  
O9K4X4 caenorhabdi  
O22186 caenorhabdi  
O6DVL4 thermobia d  
O71U37 gallus galli  
O7U7E8 synecococc  
O6DJP2 xenopus lae  
O8KXA7 chlorobium  
O92QW7 rhizobium m  
O8TRQ7 methanosarc  
O9ZCP1 rickettsia  
O8B3A4 pseudomonas  
O8ITL0 arabisidopsis  
O94A06 xenopus tto  
O6DVA5 vibrio para  
O87KJ6 xenopus lae  
O6GLN0 xenopus lae  
O81V85 bacillus an  
O8B1C8 pseudomonas  
O67164 aquilex aeo  
O83BM7 coxiella bu  
O8P2B7 streptococc  
O6GMH6 lycopersico  
O6CTU9 kluyveromyc  
O9A1A0 streptococc  
O38943 arabisidopsis  
O04440 arabisidopsis  
O751E0 oryza sativ  
O8U2K8 pyrococcus  
O37395 allomyces m  
O00052 lactobacill  
O39688 daucus caro  
O74K34 lactobacill  
O81CD6 bacillibacill  
O6NCT8 rhodospseudo  
O6XOG9 sus scrofa  
O9BT50 homo sapien  
O8EPQ2 shewanella  
O6BZX3 yarrowia li  
O72Q94 leptospira  
O72NS0 leptospira

105	7	4.0	423	2	08F7S1	08F7S1 leptoepira	178	7	4.0	749	2	0825G4	0825G4 streptomyc
106	7	4.0	423	2	08FA80	08FA80 escherichia	179	7	4.0	750	2	07S6E7	07S6E7 neurospora
107	7	4.0	426	2	031471	031471 bacillus eu	180	7	4.0	754	2	060934	060934 homo sapien
108	7	4.0	433	2	08F5M4	08F5M4 leptospira	181	7	4.0	754	2	071DM2	071DM2 homo sapien
109	7	4.0	438	2	08FJ14	08FJ14 candida gla	182	7	4.0	754	2	084LH7	084LH7 oryza sativ
110	7	4.0	438	2	08M4W3	08M4W3 zea mays (m	183	7	4.0	761	2	082634	082634 arabidopsis
111	7	4.0	440	2	06A9Q3	06A9Q3 propionibac	184	7	4.0	762	1	MUS2_HELPJ	09J114 helicobacte
112	7	4.0	441	2	084706	084706 chlamydia t	185	7	4.0	784	2	MUS2_HELPJ	025318 helicobacte
113	7	4.0	444	2	09M8N1	09M8N1 arabidopsis	186	7	4.0	787	2	0881N5	0881N5 pseudomonas
114	7	4.0	445	2	09SRV8	09SRV8 arabidopsis	187	7	4.0	835	1	STFB_CONEF	061B87 oligotroph
115	7	4.0	445	2	06A177	06A177 desulfotale	188	7	4.0	850	2	09SR05	081TP0 corynebacte
116	7	4.0	451	2	09W1F6	09W1F6 dirosophila	189	7	4.0	852	2	09P240	09SR05 arabidopsis
117	7	4.0	451	2	08R1T1	08R1T1 mus musculu	190	7	4.0	883	2	07S5F9	09P240 homo sapien
118	7	4.0	452	2	08NDM1	08NDM1 homo sapien	191	7	4.0	883	2	06K9J3	07S5F91 aethya gos
119	7	4.0	453	2	08MUX9	08MUX9 homo sapien	192	7	4.0	898	2	06K9J3	06K9J3 oryza sativ
120	7	4.0	454	2	06CTI3	06CTI3 kluyveromyc	193	7	4.0	915	2	09S7Y7	09S7Y7 arabidopsis
121	7	4.0	456	2	0972Q9	0972Q9 sulfolobus	194	7	4.0	921	2	074XT3	074XT3 yersinia pe
122	7	4.0	456	2	06KMW4	06KMW4 bacillus an	195	7	4.0	930	2	08ZBN7	08ZBN7 yersinia pe
123	7	4.0	463	2	06JEW3	06JEW3 bacillus ce	196	7	4.0	931	2	07NBN0	07NBN0 mycoplasma
124	7	4.0	463	2	081U49	081U49 bacillus an	197	7	4.0	933	2	08D1A1	08D1A1 yersinia pe
125	7	4.0	463	2	06HMC4	06HMC4 bacillus th	198	7	4.0	968	2	09JNTO	09JNTO kadiptro vi
126	7	4.0	469	2	06TQ31	06TQ31 homo sapien	199	7	4.0	978	2	P91777	P91777 pacifastacu
127	7	4.0	471	2	Q17960	Q17960 caenorhabdi	200	7	4.0	979	2	081YES	081YES homo sapien
128	7	4.0	471	2	08GMB5	08GMB5 arabidopsis	201	7	4.0	994	2	070JU3	070JU3 homo sapien
129	7	4.0	473	2	094606	094606 s jmc doma	202	7	4.0	1008	2	09H2U1	09H2U1 homo sapien
130	7	4.0	475	2	06YZC9	06YZC9 oryza sativ	203	7	4.0	1017	2	09LKV5	09LKV5 arabidopsis
131	7	4.0	478	2	09ZUL2	09ZUL2 rhizobium m	204	7	4.0	1018	2	06SHL7	06SHL7 uncultured
132	7	4.0	480	2	048705	048705 arabidopsis	205	7	4.0	1063	2	06MMJ3	06MMJ3 neurospora
133	7	4.0	491	2	09VXK6	09VXK6 dirosophila	206	7	4.0	1100	2	09M319	09M319 arabidopsis
134	7	4.0	498	2	06BPPX9	06BPPX9 debaryomyce	207	7	4.0	1101	2	07UV84	07UV84 rhodospirell
135	7	4.0	499	2	06S049	06S049 morus alba	208	7	4.0	1116	2	07RA41	07RA41 plasmodium
136	7	4.0	499	2	087275	087275 pseudomonas	209	7	4.0	1121	2	0942F3	0942F3 oryza sativ
137	7	4.0	505	2	08SV94	08SV94 elaeagnus u	210	7	4.0	1138	2	08RX85	08RX85 arabidopsis
138	7	4.0	512	2	09KM26	09KM26 vibrio chol	211	7	4.0	1140	2	06BRB6	06BRB6 debaryomyce
139	7	4.0	514	2	06VZ29	06VZ29 canarypox v	212	7	4.0	1153	2	06B1P2	06B1P2 debaryomyce
140	7	4.0	516	2	06CED6	06CED6 yarrowia li	213	7	4.0	1166	2	07Q992	07Q992 anopheles g
141	7	4.0	523	2	074HN4	074HN4 lactobacilli	214	7	4.0	1213	2	08ZKX1	08ZKX1 salmonella
142	7	4.0	532	2	08QU03	08QU03 nipah virus	215	7	4.0	1266	2	09LSH3	09LSH3 arabidopsis
143	7	4.0	532	2	091K92	091K92 nipah virus	216	7	4.0	1404	2	07TIC9	07TIC9 brachydanto
144	7	4.0	542	2	07YXQ3	07YXQ3 bordetella	217	7	4.0	1556	1	PROS_DROVI	09U6A1 dirosophila
145	7	4.0	542	2	07M647	07M647 bordetella	218	7	4.0	1656	2	09XJX8	09XJX8 streptococc
146	7	4.0	542	2	07M113	07M113 bordetella	219	7	4.0	1938	2	06S0D5	06S0D5 bacteroides
147	7	4.0	547	1	NRM1_CANPA	09X174 canis famli	220	7	4.0	1980	2	09VHD1	09VHD1 dirosophila
148	7	4.0	548	1	NRM1_BISBI	09S102 bison bison	221	7	4.0	2144	2	084MP1	084MP1 oryza sativ
149	7	4.0	548	1	NRM1_BOVIN	027981 bos taurus	222	7	4.0	2165	2	031971	031971 caenorhabdi
150	7	4.0	548	1	NRM1_BUBBU	027946 bubalus bub	223	7	4.0	3051	2	0733Y8	0733Y8 mycobacteri
151	7	4.0	548	1	NRM1_CEREL	P56436 cervus elap	224	7	4.0	3262	2	Q13788	Q13788 homo sapien
152	7	4.0	548	1	NRM1_SHEEP	P49280 ovis aries	225	7	4.0	4563	1	APB_HUMAN	P04114 homo sapien
153	7	4.0	554	2	09SFI2	09SFI2 arabidopsis	226	7	4.0	4563	2	072600	072600 homo sapien
154	7	4.0	555	1	NRM1_CHICK	P51027 gallus gall	227	7	4.0	5216	2	09VXZ5	09VXZ5 dirosophila
155	7	4.0	566	2	08MS58	08MS58 dirosophila	228	7	4.0	5233	2	09NB71	09NB71 dirosophila
156	7	4.0	588	2	08PBK0	08PBK0 xanthomonas	229	7	3.4	27	2	09GR20	09GR20 nematostell
157	7	4.0	589	2	08KMP2	08KMP2 raiibionia s	230	7	3.4	37	2	Q7RZ29	Q7RZ29 neurospora
158	7	4.0	605	1	G6P1_LEIME	P42861 leiishmania	231	7	3.4	38	2	055471	055471 human immun
159	7	4.0	612	2	09F7N4	09F7N4 gamma-prote	232	7	3.4	39	2	08K4D9	08K4D9 mus musculu
160	7	4.0	624	1	AMYG_ARKAD	P42042 arumula aden	233	7	3.4	40	2	08XEN3	08XEN3 chlorobium
161	7	4.0	628	1	YE1F_SCHPO	013879 schizosacch	234	7	3.4	50	2	08GXN8	08GXN8 arabidopsis
162	7	4.0	628	2	08XIX6	08XIX6 clostridium	235	7	3.4	53	2	08LWY0	08LWY0 laminaria d
163	7	4.0	629	2	08BQSO	08BQSO pseudomonas	236	7	3.4	53	2	08SFF7	08SFF7 tachyetaeta
164	7	4.0	639	2	06ZA03	06ZA03 oryza sativ	237	7	3.4	54	1	IOVO_LARRI	P05614 latus rldib
165	7	4.0	649	1	VARI_CHLNU	09P888 chlamydia m	238	7	3.4	55	2	08VYV2	08VYV2 anabaena sp
166	7	4.0	672	2	063HR6	063HR6 homo sapien	239	7	3.4	56	1	YISI_BACSU	07P5D5 fusobacteri
167	7	4.0	686	2	08A4X3	08A4X3 bacteroides	240	7	3.4	58	2	08RHV3	08RHV3 fusobacteri
168	7	4.0	705	2	Q731Z4	Q731Z4 treponema d	241	7	3.4	58	2	069MW2	069MW2 oryza sativ
169	7	4.0	711	1	CG10_APAAT	0911J0 arabidopsis	242	7	3.4	59	2	081ET6	081ET6 bacillus ce
170	7	4.0	711	1	CG10_APAAT	06T1F3 bos taurus	243	7	3.4	60	2	Q7M7H6	Q7M7H6 vibrio vuln
171	7	4.0	726	2	0823M0	0823M0 chlamydomophi	244	7	3.4	61	2	07MKNO	07MKNO uncultured
172	7	4.0	728	2	083HM4	083HM4 pseudomonas	245	7	3.4	61	2	09X369	09X369 bacillus an
173	7	4.0	732	2	06CAM6	06CAM6 yarrowia li	246	7	3.4	62	2	090ZJ7	090ZJ7 anguilla an
174	7	4.0	740	2	09RAD7	09RAD7 streptomyc	247	7	3.4	62	2	09DEP5	09DEP5 acophthalmu
175	7	4.0	743	2	09VWG6	09VWG6 dirosophila	248	7	3.4	63	1	V7K_BYDVP	P09517 barley yell
176	7	4.0	744	2	09ZRP5	09ZRP5 rhizobium m	249	7	3.4	63	1	06BUL0	06BUL0 debaryomyce
177	7	4.0	744	2	09ZRP5	09ZRP5 rhizobium m	250	7	3.4	63	2	06BUL0	06BUL0 debaryomyce

251	6	3.4	63	2	Q7VP05	Q7VP05 chlamydia p	324	6	3.4	91	2	08QG57	08QG57 gallus galli
252	6	3.4	65	2	Q8E1T5	Q8E1T5 escherichia p	325	6	3.4	92	1	VER_HPV27	P36825 human papill
253	6	3.4	66	2	Q8K4H2	Q8K4H2 mus musculus	326	6	3.4	92	2	Q6A20	068820 canis famli
254	6	3.4	66	2	Q9YCD4	Q9YCD4 aeropyrum p	327	6	3.4	92	2	Q7YAL5	Q7YAL5 fejevaraya
255	6	3.4	66	2	Q7LH80	Q7LH80 saccharomyc	328	6	3.4	92	2	Q7LIU7	Q7LIU7 lactobacilli
256	6	3.4	66	2	Q6B8M1	Q6B8M1 gracillaria	329	6	3.4	94	2	Q94YM4	Q94YM4 rana nigrom
257	6	3.4	68	2	Q6S022	Q6S022 aleutian m	330	6	3.4	95	1	BCP4_RAB1T	002247 oryctolagus
258	6	3.4	69	2	Q97UN9	Q97UN9 sulfolobus	331	6	3.4	95	1	Q7Y3G5	Q7Y3G5 enterobacte
259	6	3.4	70	2	Q97UN9	Q97UN9 geobacillus	332	6	3.4	95	2	Q9ZB99	Q9ZB99 rhodococcus
260	6	3.4	70	2	Q821B3	Q821B3 salmoneila	333	6	3.4	96	2	Q46626	Q46626 bos taurus
261	6	3.4	70	2	Q73115	Q73115 wolbachia p	334	6	3.4	97	2	Q7PA39	Q7PA39 rickettsia
262	6	3.4	71	1	Y698_ARCFU	Y698_ARCFU escherichia	335	6	3.4	97	2	Q7N3K9	Q7N3K9 vibriocarbdu
263	6	3.4	71	1	YDGT_ECO57	YDGT_ECO57 escherichia	336	6	3.4	97	2	Q88972	Q88972 vesicular e
264	6	3.4	71	1	YDGT_ECOL6	YDGT_ECOL6 escherichia	337	6	3.4	98	2	Q644M1	Q644M1 aneides har
265	6	3.4	71	1	YDGT_ECOL1	YDGT_ECOL1 shigella fl	338	6	3.4	99	2	Q9T286	Q9T286 caenorhabdi
266	6	3.4	71	1	YDGT_SHIFL	YDGT_SHIFL salmoneila	339	6	3.4	100	2	Q82165	Q82165 arabisdopsis
267	6	3.4	71	2	Q8XGJ8	Q8XGJ8 salmoneila	340	6	3.4	100	2	Q9LJV7	Q9LJV7 arabisdopsis
268	6	3.4	71	2	Q7COK5	Q7COK5 salmoneila	341	6	3.4	100	2	Q6D9N2	Q6D9N2 erwania car
269	6	3.4	71	2	Q9UUI7	Q9UUI7 neisseria m	342	6	3.4	100	2	Q9H1P4	Q9H1P4 thermoplaem
270	6	3.4	73	2	Q21096	Q21096 eurythenes	343	6	3.4	102	2	Q9H1P4	Q9H1P4 vesicular e
271	6	3.4	73	2	Q21096	Q21096 eurythenes	344	6	3.4	102	2	Q88975	Q88975 vesicular e
272	6	3.4	74	2	Q8XK15	Q8XK15 bacillus an	345	6	3.4	102	2	Q88976	Q88976 candida gla
273	6	3.4	74	2	Q9XGM1	Q9XGM1 klebsiella	346	6	3.4	103	2	Q6FLQ1	Q6FLQ1 trypanosoma
274	6	3.4	74	2	Q6E2J8	Q6E2J8 bacillus an	347	6	3.4	104	2	Q8WPT8	Q8WPT8 trypanosoma
275	6	3.4	75	2	Q72295	Q72295 caenorhabdi	348	6	3.4	104	2	Q8CAD9	Q8CAD9 arthrobacte
276	6	3.4	75	2	Q853Q4	Q853Q4 mycobacteri	349	6	3.4	104	2	Q8BD48	Q8BD48 synechococ
277	6	3.4	75	2	Q6LAL9	Q6LAL9 salmoneila	350	6	3.4	106	2	Q8BNC2	Q8BNC2 mus musculu
278	6	3.4	75	2	Q48209	Q48209 drosophila	351	6	3.4	107	2	Q8BNC2	Q8BNC2 mus musculu
279	6	3.4	76	2	Q48210	Q48210 drosophila	352	6	3.4	108	1	SV19_MOUSE	SV19_MOUSE
280	6	3.4	76	2	Q48211	Q48211 drosophila	353	6	3.4	108	2	Q9UX33	Q9UX33 sulfolobus
281	6	3.4	76	2	Q48212	Q48212 drosophila	354	6	3.4	108	2	Q6RV30	Q6RV30 chironomus
282	6	3.4	76	2	Q48213	Q48213 drosophila	355	6	3.4	108	2	Q7RT15	Q7RT15 plasmodium
283	6	3.4	76	2	Q48214	Q48214 drosophila	356	6	3.4	108	2	Q7XP13	Q7XP13 oryza sativ
284	6	3.4	76	2	Q48215	Q48215 drosophila	357	6	3.4	108	2	Q7NDB2	Q7NDB2 mus musculu
285	6	3.4	76	2	Q48216	Q48216 drosophila	358	6	3.4	110	1	VL1_PVLT	VL1_PVLT
286	6	3.4	76	2	Q48217	Q48217 drosophila	359	6	3.4	110	2	Q9HH88	Q9HH88 sulfolobus
287	6	3.4	76	2	Q48218	Q48218 drosophila	360	6	3.4	110	2	Q8H7A7	Q8H7A7 arabisdopsis
288	6	3.4	76	2	Q48219	Q48219 drosophila	361	6	3.4	110	2	Q7NUP5	Q7NUP5 chromobacte
289	6	3.4	76	2	Q48220	Q48220 scaptomyza	362	6	3.4	110	2	Q6D2M2	Q6D2M2 erwania car
290	6	3.4	76	2	Q48222	Q48222 drosophila	363	6	3.4	111	2	Q9VAR5	Q9VAR5 drosophila
291	6	3.4	76	2	Q48223	Q48223 drosophila	364	6	3.4	111	2	Q7NDB2	Q7NDB2 gloebacter
292	6	3.4	76	2	Q48224	Q48224 drosophila	365	6	3.4	112	2	Q9D634	Q9D634 m mus muscu
293	6	3.4	76	2	Q75TG6	Q75TG6 bacillus st	366	6	3.4	113	2	Q7Z6J7	Q7Z6J7 homo sapien
294	6	3.4	76	2	Q8GEL9	Q8GEL9 pseudomonas	367	6	3.4	114	2	Q9RK45	Q9RK45 streptomyce
295	6	3.4	76	2	P72914	P72914 synechocyst	368	6	3.4	114	2	Q8UD09	Q8UD09 agrobacteri
296	6	3.4	76	2	Q8UJ39	Q8UJ39 agrobacteri	369	6	3.4	115	2	Q7RWE0	Q7RWE0 neurospora
297	6	3.4	76	2	Q9ZT13	Q9ZT13 neisseria m	370	6	3.4	115	2	Q6UY24	Q6UY24 homo sapien
298	6	3.4	77	2	Q6BGN6	Q6BGN6 debaryomyce	371	6	3.4	115	2	P95435	P95435 pseudomonas
299	6	3.4	77	2	Q7CC99	Q7CC99 anopheles g	372	6	3.4	115	2	Q7ZB07	Q7ZB07 desulfovibr
300	6	3.4	79	2	Q6UAT6	Q6UAT6 bacterioph	373	6	3.4	116	2	Q8KX08	Q8KX08 proteus mir
301	6	3.4	79	2	Q9MB10	Q9MB10 bacterioph	374	6	3.4	116	2	Q73NB7	Q73NB7 treponema d
302	6	3.4	79	2	Q8A1S7	Q8A1S7 bacteroides	375	6	3.4	116	2	Q6D330	Q6D330 erwania car
303	6	3.4	79	2	YSPF_SHIFL	YSPF_SHIFL shigella fl	376	6	3.4	116	2	Q9YPA43	Q9YPA43 aeropyrum p
304	6	3.4	80	1	Q24195	Q24195 oryza sativ	377	6	3.4	117	2	Q8YV08	Q8YV08 anabaena sp
305	6	3.4	82	2	Q7XAW4	Q7XAW4 brasica ra	378	6	3.4	117	2	Q6F6Y7	Q6F6Y7 acinetobact
306	6	3.4	82	2	Q83D70	Q83D70 coxiella bu	379	6	3.4	117	2	Q7U5E0	Q7U5E0 synechococ
307	6	3.4	82	2	Q7LIJ8	Q7LIJ8 lactobacilli	380	6	3.4	117	2	Q9XN10	Q9XN10 vibrio chol
308	6	3.4	83	1	PSAK_CYACA	PSAK_CYACA cyanidium c	381	6	3.4	118	2	Q9YR16	Q9YR16 aeropyrum p
309	6	3.4	84	1	Q8ZGN6	Q8ZGN6 yersteinia pe	382	6	3.4	118	2	Q84FR3	Q84FR3 uncultured
310	6	3.4	86	2	Q98A51	Q98A51 rhizobium 1	383	6	3.4	119	2	Q84F05	Q84F05 uncultured
311	6	3.4	86	2	Q42211	Q42211 arabisdopsis	384	6	3.4	119	2	Q84F06	Q84F06 uncultured
312	6	3.4	88	2	Q30435	Q30435 enterococcu	385	6	3.4	119	2	Q84F07	Q84F07 uncultured
313	6	3.4	88	2	Q8NUT0	Q8NUT0 staphylococ	387	6	3.4	119	2	Q84F08	Q84F08 uncultured
314	6	3.4	88	2	Q99RH6	Q99RH6 staphylococ	388	6	3.4	121	2	Q9OC24	Q9OC24 periplaneta
315	6	3.4	88	2	Q7A3P1	Q7A3P1 staphylococ	389	6	3.4	122	1	RL14_CHLMT	RL14_CHLMT chlamydia m
316	6	3.4	88	2	Q6G6L4	Q6G6L4 staphylococ	390	6	3.4	122	1	RL14_CHLMT	RL14_CHLMT chlamydia p
317	6	3.4	88	2	Q90YF5	Q90YF5 pleuronacte	391	6	3.4	122	1	Y202_MYCGB	Y202_MYCGB
318	6	3.4	89	1	Q90YF5	Q90YF5 xenopus lae	392	6	3.4	122	1	Q817Q8	Q817Q8 arabisdopsis
319	6	3.4	89	1	Q90YF5	Q90YF5 xenopus lae	393	6	3.4	122	2	Q73FR3	Q73FR3 wolbachia p
320	6	3.4	89	1	Q90YF5	Q90YF5 xenopus lae	394	6	3.4	122	2	Q824P1	Q824P1 chlamydomophi
321	6	3.4	90	2	Q7YX02	Q7YX02 mycobacteri	395	6	3.4	122	2	Q6M553	Q6M553 parachlamyid
322	6	3.4	90	2	Q7YX02	Q7YX02 mycobacteri	396	6	3.4	122	2	Q6M553	Q6M553 parachlamyid
323	6	3.4	91	2	Q8LWAO	Q8LWAO otus brucei	397	6	3.4	122	2	Q6M553	Q6M553 parachlamyid

397	6	3.4	123	2	Q7PN37	Q7PN37 anopheles g	470	6	3.4	138	2	Q8B186	Q8B186 san miguel
398	6	3.4	123	2	Q30533	Q30533 pseudomonas	471	6	3.4	139	2	Q6BT83	Q6BT83 debaryomyce
399	6	3.4	123	2	Q730V1	Q730V1 bacillus ce	472	6	3.4	139	2	Q6XH06	Q6XH06 drosophila
400	6	3.4	123	2	Q91329	Q91329 pseudomonas	473	6	3.4	139	2	Q9XK38	Q9XK38 drosophila
401	6	3.4	124	1	YBF3 YEAST	YBF3 baccharomyc	474	6	3.4	139	2	Q9XK53	Q9XK53 drosophila
402	6	3.4	124	2	Q7QVD9	Q7QVD9 giardia lam	475	6	3.4	139	2	Q9XN65	Q9XN65 drosophila
403	6	3.4	124	2	Q88974	Q88974 vesicular e	476	6	3.4	139	2	Q9XN67	Q9XN67 drosophila
404	6	3.4	125	2	Q970K1	Q970K1 sulfolobus	477	6	3.4	139	2	Q9XN67	Q9XN67 drosophila
405	6	3.4	125	2	Q9LH14	Q9LH14 arabidopsis	478	6	3.4	139	2	Q9XN68	Q9XN68 drosophila
406	6	3.4	125	2	Q66GZ4	Q66GZ4 xenopus lae	479	6	3.4	139	2	Q9XN69	Q9XN69 drosophila
407	6	3.4	126	2	Q9G919	Q9G919 rana chensi	480	6	3.4	139	2	Q9XN70	Q9XN70 drosophila
408	6	3.4	126	2	Q8CT85	Q8CT85 staphylococ	481	6	3.4	139	2	Q9XN71	Q9XN71 drosophila
409	6	3.4	126	2	Q9PDL3	Q9PDL3 xyella fas	482	6	3.4	139	2	Q9XN85	Q9XN85 drosophila
410	6	3.4	127	2	Q9ZU00	Q9ZU00 arabidopsis	483	6	3.4	139	2	Q9XN86	Q9XN86 drosophila
411	6	3.4	127	2	Q64VZ6	Q64VZ6 bacteroides	484	6	3.4	139	2	Q9XN87	Q9XN87 drosophila
412	6	3.4	127	2	Q8UT13	Q8UT13 agrobacteri	485	6	3.4	139	2	Q9XN88	Q9XN88 drosophila
413	6	3.4	127	2	Q97JK9	Q97JK9 clostridium	486	6	3.4	139	2	Q33304	Q33304 mycobacteri
414	6	3.4	127	2	Q7A1C1	Q7A1C1 staphylococ	487	6	3.4	139	2	Q735J7	Q735J7 bacillus ce
415	6	3.4	127	2	Q7A2T4	Q7A2T4 staphylococ	488	6	3.4	139	2	Q8B185	Q8B185 san miguel
416	6	3.4	127	2	Q7A6I2	Q7A6I2 staphylococ	489	6	3.4	140	2	Q65NM6	Q65NM6 bacillus 11
417	6	3.4	127	2	Q88S06	Q88S06 lactobacill	490	6	3.4	141	1	YCB6_PSEDE	YCB6_PSEDE
418	6	3.4	127	2	Q9ZNG7	Q9ZNG7 staphylococ	491	6	3.4	141	2	Q99152	Q99152 pseudomonas
419	6	3.4	127	2	Q6GAX3	Q6GAX3 staphylococ	492	6	3.4	141	2	Q9YE51	Q9YE51 aeropyrum p
420	6	3.4	127	2	Q6GID5	Q6GID5 staphylococ	493	6	3.4	141	2	Q9HXQ3	Q9HXQ3 pseudomonas
421	6	3.4	128	2	Q8TM72	Q8TM72 methanosarc	494	6	3.4	142	1	HBA_CARAU	HBA_CARAU
422	6	3.4	128	2	Q6WFF6	Q6WFF6 human immun	495	6	3.4	143	2	Q8RFM9	Q8RFM9 fusobacteri
423	6	3.4	129	2	Q7YU27	Q7YU27 trypanosoma	496	6	3.4	143	2	Q9ZMU9	Q9ZMU9 helicobacte
424	6	3.4	129	2	P95131	P95131 mycobacteri	497	6	3.4	143	2	Q8TH84	Q8TH84 ctenopharym
425	6	3.4	129	2	Q7RXJ5	Q7RXJ5 mycobacteri	498	6	3.4	143	2	Q8TH90	Q8TH90 carassius a
426	6	3.4	131	2	Q7RZ15	Q7RZ15 neurospora	499	6	3.4	144	1	CND8_HUMAN	CND8_HUMAN
427	6	3.4	131	2	Q75J22	Q75J22 dictyosteli	500	6	3.4	144	2	Q6KD68	Q6KD68 escherichia
428	6	3.4	131	2	Q6VAG5	Q6VAG5 bacteroides	501	6	3.4	144	2	Q7VJR6	Q7VJR6 helicobacte
429	6	3.4	131	2	Q6WLX3	Q6WLX3 bdellovibri	502	6	3.4	144	2	Q8E514	Q8E514 streptococc
430	6	3.4	133	2	Q9YDU6	Q9YDU6 aeropyrum p	503	6	3.4	144	2	Q8EKK4	Q8EKK4 oceanobacill
431	6	3.4	135	2	Q6FUG3	Q6FUG3 homo saplen	504	6	3.4	144	2	Q9ANE2	Q9ANE2 bradyrhizob
432	6	3.4	135	2	Q7RUV7	Q7RUV7 prochloroco	505	6	3.4	145	2	Q8VAST	Q8VAST agrobacteri
433	6	3.4	137	2	Q8NRH4	Q8NRH4 corynebacte	506	6	3.4	145	2	Q8FV83	Q8FV83 bruceella su
434	6	3.4	137	2	Q89U75	Q89U75 bradyrhizob	507	6	3.4	145	2	Q6D2C8	Q6D2C8 erwina car
435	6	3.4	138	2	Q85AR0	Q85AR0 drosophila	508	6	3.4	145	2	Q8BY58	Q8BY58 mus masculu
436	6	3.4	138	2	Q85AR1	Q85AR1 drosophila	509	6	3.4	146	2	Q8J1X8	Q8J1X8 coccidioides
437	6	3.4	138	2	Q85T71	Q85T71 drosophila	510	6	3.4	146	2	Q7X650	Q7X650 oryza sativ
438	6	3.4	138	2	Q85T72	Q85T72 drosophila	511	6	3.4	146	2	Q9M719	Q9M719 arabidopsis
439	6	3.4	138	2	Q85T73	Q85T73 drosophila	512	6	3.4	146	2	Q8P866	Q8P866 xanthomonas
440	6	3.4	138	2	Q85T74	Q85T74 drosophila	513	6	3.4	146	2	Q8PJL5	Q8PJL5 xanthomonas
441	6	3.4	138	2	Q85T75	Q85T75 drosophila	514	6	3.4	147	1	HPK_PORCI	HPK_PORCI porphyromon
442	6	3.4	138	2	Q85T77	Q85T77 drosophila	515	6	3.4	148	2	Q86WT5	Q86WT5 homo saplen
443	6	3.4	138	2	Q85T78	Q85T78 drosophila	516	6	3.4	148	2	Q9VBG7	Q9VBG7 drosophila
444	6	3.4	138	2	Q85T79	Q85T79 drosophila	517	6	3.4	148	2	Q6YRL5	Q6YRL5 oryza sativ
445	6	3.4	138	2	Q85T80	Q85T80 drosophila	518	6	3.4	148	2	Q821L9	Q821L9 streptomyce
446	6	3.4	138	2	Q85T81	Q85T81 drosophila	519	6	3.4	149	2	Q09784	Q09784 san miguel
447	6	3.4	138	2	Q85T82	Q85T82 drosophila	520	6	3.4	149	2	Q09787	Q09787 san miguel
448	6	3.4	138	2	Q85T83	Q85T83 drosophila	521	6	3.4	149	2	Q8UZL1	Q8UZL1 bovine cali
449	6	3.4	138	2	Q85T84	Q85T84 drosophila	522	6	3.4	150	2	Q8PFH1	Q8PFH1 xanthomonas
450	6	3.4	138	2	Q85T86	Q85T86 drosophila	523	6	3.4	150	2	Q09736	Q09736 cetacean ca
451	6	3.4	138	2	Q85T87	Q85T87 drosophila	524	6	3.4	150	2	Q09775	Q09775 primate cal
452	6	3.4	138	2	Q85T88	Q85T88 drosophila	525	6	3.4	150	2	Q09776	Q09776 reptile cal
453	6	3.4	138	2	Q85T89	Q85T89 drosophila	526	6	3.4	150	2	Q09785	Q09785 san miguel
454	6	3.4	138	2	Q85T91	Q85T91 drosophila	527	6	3.4	150	2	Q09786	Q09786 san miguel
455	6	3.4	138	2	Q85T92	Q85T92 drosophila	528	6	3.4	151	2	Q9VBF0	Q9VBF0 drosophila
456	6	3.4	138	2	Q85T93	Q85T93 drosophila	529	6	3.4	151	2	Q9CF70	Q9CF70 arabidopsis
457	6	3.4	138	2	Q85T96	Q85T96 drosophila	530	6	3.4	151	2	Q9EF07	Q9EF07 arabidopsis
458	6	3.4	138	2	Q85T98	Q85T98 drosophila	531	6	3.4	152	2	Q7PJ06	Q7PJ06 anopheles g
459	6	3.4	138	2	Q9TAV8	Q9TAV8 drosophila	532	6	3.4	152	2	Q84JN5	Q84JN5 oryza sativ
460	6	3.4	138	2	Q9TAV9	Q9TAV9 drosophila	533	6	3.4	152	2	Q6LIB7	Q6LIB7 oligotropa
461	6	3.4	138	2	Q9TAW0	Q9TAW0 drosophila	534	6	3.4	152	2	Q80H39	Q80H39 agrobacteri
462	6	3.4	138	2	Q9TAW1	Q9TAW1 drosophila	535	6	3.4	153	1	RISC_ARCFU	RISC_ARCFU
463	6	3.4	138	2	Q9TAW2	Q9TAW2 drosophila	536	6	3.4	153	2	Q647X1	Q647X1 uncultured
464	6	3.4	138	2	Q9XJY8	Q9XJY8 drosophila	537	6	3.4	153	2	Q6LIV3	Q6LIV3 drosophila
465	6	3.4	138	2	Q9XK12	Q9XK12 drosophila	538	6	3.4	153	2	Q8P3Z0	Q8P3Z0 xanthomonas
466	6	3.4	138	2	Q9XN53	Q9XN53 drosophila	539	6	3.4	153	2	Q9AAS8	Q9AAS8 caulobacter
467	6	3.4	138	2	Q9XN54	Q9XN54 drosophila	540	6	3.4	153	2	Q90068	Q90068 feline immu
468	6	3.4	138	2	Q9XN55	Q9XN55 drosophila	541	6	3.4	154	2	Q9HLS6	Q9HLS6 thermoplasma
469	6	3.4	138	2	Q8BJJ3	Q8BJJ3 shewanella	542	6	3.4	154	2	Q8YHH9	Q8YHH9 bruceella me

543	6	3.4	154	2	06G0D3	06G0D3 bruceella su	616	6	3.4	170	2	07MC16	07mc16 vibrio vuln
544	6	3.4	154	2	06C238	06c238 erwania car	617	6	3.4	170	2	06D5K2	06d5k2 vibrio vuln
545	6	3.4	155	2	08XM89	08xm89 clostridium	618	6	3.4	171	1	1126_HUMAN	09npb9 homo sapien
546	6	3.4	155	2	06UG70	06ug70 sulfolobus	619	6	3.4	172	1	0824V3	0824v3 chlamydomo
547	6	3.4	156	2	08SCM0	08scm0 pseudomonas	620	6	3.4	172	2	091749	091749 pseudomonas
548	6	3.4	156	2	09S6G3	09s6g3 streptococc	621	6	3.4	173	1	BURS_DROME	09y4d83 dirosophila
549	6	3.4	156	2	09S6G4	09s6g4 streptococc	622	6	3.4	173	1	CD3D_MOUSE	09k4235 mus musculu
550	6	3.4	156	2	09S6G4	09s6g4 streptococc	623	6	3.4	173	1	YKNI_YEAST	P36067 saccharomyc
551	6	3.4	157	1	09DHV7	09dhv7 yaba-like d	624	6	3.4	173	1	07RNT2	07rnt2 plasmidum
552	6	3.4	157	1	LSPA_HELPY	Lspa_helpy	625	6	3.4	173	2	06T7L1	06t7l1 oryza sativ
553	6	3.4	157	2	06L3M7	06l3m7 solanum dem	626	6	3.4	173	2	06Q8V6	06q8v6 uncultured
554	6	3.4	157	2	09S006	09s006 helicobacte	627	6	3.4	173	2	07WX23	07wx23 alcaligenes
555	6	3.4	157	2	082106	082106 streptomyc	628	6	3.4	173	2	08RBF3	08rbf3 thermoaer
556	6	3.4	157	2	08A305	08a305 bacterioides	629	6	3.4	173	2	08RBF3	08rbf3 thermoaer
557	6	3.4	157	2	010694	010694 avian papil	630	6	3.4	173	2	083E94	083e94 coxiella bu
558	6	3.4	158	1	RK12_ORYSA	022386 oryza sativ	631	6	3.4	173	2	06S398	06s398 mus musculu
559	6	3.4	158	2	09CSA0	09csa0 ovine aries	632	6	3.4	173	2	06S398	06s398 bovine call
560	6	3.4	158	2	09SCS5	09scs5 arabidopsis	633	6	3.4	173	2	087003	087003 skunk calic
561	6	3.4	158	2	09EMB3	09emb3 streptomyc	634	6	3.4	173	2	087007	087007 skunk calic
562	6	3.4	158	2	08NXX0	08nxx0 staphylococ	635	6	3.4	173	2	087018	087018 skunk calic
563	6	3.4	159	1	06N7D7	06n7d7 rhodopseudo	636	6	3.4	173	2	088174	088174 san miguel
564	6	3.4	159	1	VT3A_CAPVI	P48276 cyanophora	637	6	3.4	173	2	088176	088176 san miguel
565	6	3.4	159	1	YC36_CVAPA	P48276 cyanophora	638	6	3.4	173	2	088183	088183 san miguel
566	6	3.4	159	2	06SEF9	06sef9 verticillium	639	6	3.4	173	2	088965	088965 vesicular e
567	6	3.4	159	2	06ESF0	06esf0 verticillium	640	6	3.4	173	2	088973	088973 homo sapien
568	6	3.4	159	2	08YVL5	08yvl5 anabaena sp	641	6	3.4	174	2	08RX55	08rx55 homo sapien
569	6	3.4	159	2	08YVL5	08yvl5 anabaena sp	642	6	3.4	174	2	092VRL	092vrl rhizobium m
570	6	3.4	160	2	0910J8	0910j8 lumpy skin	643	6	3.4	174	2	087JY7	087jy7 vibrio para
571	6	3.4	160	2	08U2B6	08u2b6 pyrococcus	644	6	3.4	175	2	06ZS55	06z555 homo sapien
572	6	3.4	160	2	0610T4	0610t4 microphilus	645	6	3.4	175	2	08E1F2	08e1f2 streptococc
573	6	3.4	160	2	07RP05	07rp05 plasmodium	646	6	3.4	175	2	08B6X0	08b6x0 streptococc
574	6	3.4	160	2	08PNC3	08pnc3 xanthomonas	647	6	3.4	176	2	07DMN7	07dmn7 crassostrea
575	6	3.4	160	2	08CYC2	08cy22 bruceella me	648	6	3.4	176	2	07IDQ8	07idq8 lobochlamys
576	6	3.4	161	1	08FOX7	08fox7 corynebacte	649	6	3.4	176	2	07ZS24	07zsz24 tetraodon n
577	6	3.4	161	1	TATE_SPRCO	09h157 thermoplasma	650	6	3.4	177	1	IL19_HUMAN	09und0 homo sapien
578	6	3.4	161	2	09HL57	09hl57 thermoplasma	651	6	3.4	177	1	06FA57	06fa57 pluteella xy
579	6	3.4	161	2	097LL4	097ll4 clostridium	652	6	3.4	178	1	COXZ_RICPR	09zdm3 rickettsia
580	6	3.4	161	2	088439	088439 strewberry	653	6	3.4	178	2	032584	032584 escherichia
581	6	3.4	162	1	PHAI_PREDI	P07122 fremyella d	654	6	3.4	178	2	08FR96	08fr96 corynebacte
582	6	3.4	162	1	PHAS_PSEB9	052452 pseudanaba	655	6	3.4	178	2	09XP85	09xp85 vibrio chol
583	6	3.4	162	1	PHAS_PSEB9	P14876 fremyella d	656	6	3.4	180	2	08PVJ2	08pvj2 methanosarc
584	6	3.4	163	1	LSPA_HELPJ	09zmx3 helicobacte	657	6	3.4	180	2	06UB88	06ub88 staphylococc
585	6	3.4	163	2	06ZRX9	06zrx9 homo sapien	658	6	3.4	180	2	07CS40	07cs40 agrobacteri
586	6	3.4	163	2	07PFJ0	07pfj0 anopheles g	659	6	3.4	180	2	08XRY8	08xry8 ralteonla s
587	6	3.4	163	2	08H3A5	08h3a5 oryza sativ	660	6	3.4	180	2	08CKX9	08ckx9 oceanobacil
588	6	3.4	163	2	07TTN0	07ttn0 haemophilus	661	6	3.4	181	2	07T311	07t311 coccidioid
589	6	3.4	163	2	09CQ09	09cq09 m mus muscu	662	6	3.4	181	2	AG19_COCCIM	09x826 streptomyc
590	6	3.4	163	2	084686	084686 primace cal	663	6	3.4	181	2	09X826	09x826 streptomyc
591	6	3.4	164	2	085988	085988 sphingomonas	664	6	3.4	181	2	088187	088187 san miguel
592	6	3.4	164	2	07BKRO	07bkro synecocyst	665	6	3.4	182	2	07Q098	07q098 giardia lam
593	6	3.4	164	2	09KJH5	09kjh5 synecocyst	666	6	3.4	182	2	0902G7	09u2g7 caenorhabdi
594	6	3.4	165	2	06STB6	06stb6 cereal yell	667	6	3.4	182	2	08XHG7	08xhg7 clostridium
595	6	3.4	165	2	07NMB7	07nm77 gloebacter	668	6	3.4	182	2	08U878	08u878 agrobacteri
596	6	3.4	166	2	08Y9D0	08y9d0 listeria mo	669	6	3.4	183	2	045250	045250 caenorhabdi
597	6	3.4	166	2	092B50	092b50 listeria in	670	6	3.4	183	2	08W760	08w760 bacterioph
598	6	3.4	166	2	0722U8	0722u8 listeria mo	671	6	3.4	183	2	08W760	08w760 bacterioph
599	6	3.4	166	2	07VGR8	07vgr8 prochloroco	672	6	3.4	183	2	08R2X1	08r2x1 oryza sativ
600	6	3.4	167	1	CD3D_SHEEP	081d48 ovine aries	673	6	3.4	183	2	0921D2	0921d2 rickettsia
601	6	3.4	167	1	08LDI5	08ldi5 arabidopsis	674	6	3.4	184	1	0822U3	0822u3 chlamydomo
602	6	3.4	167	2	09SACS	09sacs arabidopsis	675	6	3.4	184	1	TR17_HUMAN	06pe46 homo sapien
603	6	3.4	167	2	07W063	07w063 bordetella	676	6	3.4	184	2	06PEZ6	06pe46 homo sapien
604	6	3.4	167	2	07W358	07w358 bordetella	677	6	3.4	184	2	06NEZ6	06ne46 rhodopseudo
605	6	3.4	167	2	07WFS6	07wfs6 bordetella	678	6	3.4	184	2	07UUX6	07uux6 rhodopseu
606	6	3.4	168	2	08SNP7	08snf7 xiphophorus	679	6	3.4	184	2	08ENH8	08enh8 oceanobacil
607	6	3.4	168	2	08SNP3	08sn33 xiphophorus	680	6	3.4	185	1	AP10_HUMAN	09umj3 homo sapien
608	6	3.4	168	2	08SNP4	08sn44 xiphophorus	681	6	3.4	185	1	AP10_MOUSE	08k2h6 mus musculu
609	6	3.4	168	2	08SNP5	08sn55 xiphophorus	682	6	3.4	185	1	VG16_HAEIN	P71387 haemophilus
610	6	3.4	168	2	08SNP6	08sn66 xiphophorus	683	6	3.4	185	2	09VAF7	09vap7 drosoophila
611	6	3.4	168	2	036423	036423 alcelaphine	684	6	3.4	185	2	09ZWF4	09zwf4 oryza sativ
612	6	3.4	169	1	YCEI_PSAAB	090342 cercopithe	685	6	3.4	185	2	072T61	072t61 leptospira
613	6	3.4	169	1	YCEI_PSAAB	09huv9 pseudomonas	686	6	3.4	185	2	074IK7	074ik7 iactobacilli
614	6	3.4	169	2	08SNT7	08snt7 xiphophorus	687	6	3.4	186	2	08P292	08p292 leptospira
615	6	3.4	169	2	068613	068613 synecococc	688	6	3.4	186	2	08NPE4	08np64 corynebacte

689	3.4	186	2	Q7ND30	Q7nd30 gloeobacter	762	6	3.4	200	2	Q66CW4	Q66cw4 yersinia ps
690	3.4	186	2	Q6BJ57	Q6bj57 gopherus po	763	6	3.4	200	2	Q90YF1	Q90yf1 pleuronecte
691	3.4	187	2	Q6X2P4	Q6x2p4 verticordia	764	6	3.4	202	1	R813_MOUSE	Q9dd01 mus musculu
692	3.4	187	2	Q6X2F7	Q6x2f7 chemelauctu	765	6	3.4	202	1	V357_CAMBE	Q9p1e4 campylobact
693	3.4	187	2	Q6X2F8	Q6x2f8 chemelauctu	766	6	3.4	202	2	Q617D0	Q617d0 pyrobaculum
694	3.4	187	2	Q9HVS2	Q9hvs2 pseudomonas	767	6	3.4	202	2	Q703Z8	Q703z8 thermoprote
695	3.4	188	1	COX2_RICCN	Q92112 rickettsia	768	6	3.4	202	2	Q970X9	Q970x9 sulfolobus
696	3.4	188	2	O27534	O27534 mechanobact	769	6	3.4	202	2	Q6EQ71	Q6eq71 oryza sativ
697	3.4	188	2	Q6CGN2	Q6cgn2 yarrowia li	770	6	3.4	202	2	Q9RG18	Q9rg18 bacteroides
698	3.4	188	2	Q7YX04	Q7yx04 caenorhabdi	771	6	3.4	202	2	Q9RPA8	Q9rpa8 streptomyc
699	3.4	188	2	Q6AVC7	Q6avc7 oryza sativ	772	6	3.4	202	2	Q64Y58	Q64y58 bacteroides
700	3.4	188	2	Q7PBB0	Q7pbb0 rickettsia	773	6	3.4	203	1	GTS1_BLAG	Q18598 blattella g
701	3.4	188	2	Q72Y14	Q72y14 bacillus ce	774	6	3.4	203	1	HIS5_THETN	Q81883 thermomater
702	3.4	188	2	Q816S6	Q816s6 bacillus ce	775	6	3.4	203	2	Q681I2	Q681i2 arbidopais
703	3.4	188	2	Q81KX2	Q81kx2 bacillus an	776	6	3.4	203	2	Q7AB11	Q7ab11 escherichia
704	3.4	188	2	Q6HBO2	Q6hbq2 bacillus th	777	6	3.4	203	2	Q7VP8	Q7vp8 bordetella
705	3.4	188	2	Q6HCD8	Q6hcd8 bacillus th	778	6	3.4	203	2	Q7MAS5	Q7mas5 bordetella
706	3.4	188	2	Q8R334	Q8r334 mus musculu	779	6	3.4	203	2	Q7WY14	Q7wy14 bordetella
707	3.4	189	2	Q8KD20	Q8kd20 chlorobium	780	6	3.4	204	1	COAT_BYDVN	P27578 barley yell
708	3.4	189	2	Q8PF77	Q8pf77 xanthomonas	781	6	3.4	204	1	GBIR_HUMAN	P52565 homo sapien
709	3.4	189	2	Q8U5G7	Q8u5g7 agrobacteri	782	6	3.4	204	2	Q8TQ03	Q8tcq3 mechanosarc
710	3.4	190	2	Q6DHH7	Q6dhh7 brachydantio	783	6	3.4	204	2	Q8VZ03	Q8vzq3 arabidopsis
711	3.4	191	2	Q9LH47	Q9lh47 arabidopsis	784	6	3.4	204	2	Q8SHH9	Q8shh9 arabidopsis
712	3.4	191	2	Q7NM10	Q7nm10 chromobacte	785	6	3.4	204	2	Q8X819	Q8x819 escherichia
713	3.4	192	1	G1DB_MYCGE	P47620 mycoplasma	786	6	3.4	204	2	Q91ZF3	Q91zf3 cereal yell
714	3.4	192	2	P95975	P95975 sulfolobus	787	6	3.4	206	1	NO21_SOYBN	P16313 glycine max
715	3.4	192	2	Q6L012	Q6l012 picophilus	788	6	3.4	207	1	PR1_HYPMO	P33395 hyppochthalm
716	3.4	192	2	Q6C9M1	Q6c9m1 yarrowia li	789	6	3.4	207	2	Q7PL02	Q7pl02 anophelies g
717	3.4	192	2	Q7XUW7	Q7xuw7 oryza sativ	790	6	3.4	207	2	Q9ABCI	Q9abp1 desulfitoba
718	3.4	192	2	Q52373	Q52373 pseudomonas	791	6	3.4	207	2	Q8RC20	Q8rc20 chlorobium
719	3.4	192	2	Q7V0V4	Q7vov4 prochloroco	792	6	3.4	208	2	Q7MSQ4	Q7mq4 wolfinella s
720	3.4	193	2	Q8WYU3	Q8wyu3 homo sapien	793	6	3.4	208	2	Q6IGL9	Q6igl9 arabidophila
721	3.4	193	2	Q9RX05	Q9rx05 deinococcus	794	6	3.4	208	2	Q666F9	Q666f9 vibrio chol
722	3.4	194	1	PTH_PASMU	P57820 pasteurella	795	6	3.4	208	2	Q8X0S0	Q8x0s0 ralsstonia s
723	3.4	194	2	Q8IQ56	Q8iq56 dirosophila	796	6	3.4	210	2	Q95XL4	Q95xl4 caenorhabdi
724	3.4	194	2	Q8J9A5	Q8j9a5 gliosina mo	797	6	3.4	210	2	Q24557	Q24557 zea mays (m
725	3.4	194	2	Q8LBB9	Q8lbb9 arabidopsis	798	6	3.4	210	2	Q89ZA2	Q89za2 bacteroides
726	3.4	194	2	Q6Z366	Q6z366 oryza sativ	799	6	3.4	211	2	Q8IMY2	Q8imy2 dirosophila
727	3.4	194	2	Q6SD84	Q6sd84 arabidopsis	800	6	3.4	211	2	Q7PGA2	Q7pga2 anophelies g
728	3.4	194	2	Q82BZ1	Q82bz1 streptomyc	801	6	3.4	212	2	Q67MM8	Q67mm8 oryza sativ
729	3.4	195	2	Q97416	Q97416 sulfolobus	802	6	3.4	212	2	Q9FK98	Q9fk98 arabidopsis
730	3.4	195	2	Q9NT21	Q9nt21 homo sapien	803	6	3.4	212	2	Q6G591	Q6g591 bartonella
731	3.4	195	2	Q8MUR9	Q8mur9 anophelies g	804	6	3.4	213	1	YMO6_YEAST	Q04477 saccharomyc
732	3.4	195	2	Q7YT05	Q7yfq5 caenorhabdi	805	6	3.4	213	2	Q8YNH8	Q8ynh8 anabaena sp
733	3.4	195	2	Q7F2F2	Q7f2f2 oryza sativ	806	6	3.4	214	2	Q8PUU0	Q8puu0 mechanosarc
734	3.4	196	2	Q9YUM4	Q9yum4 dirosophila	807	6	3.4	214	2	Q05387	Q05387 saccharomyc
735	3.4	196	2	Q44751	Q44751 borrelia bu	808	6	3.4	214	2	Q6ST01	Q6std1 manheimia
736	3.4	196	2	Q6LRW7	Q6lrw7 photobacter	809	6	3.4	214	2	Q72B98	Q72b98 desulfovibr
737	3.4	196	2	Q8DCM4	Q8dcm4 vibrio vuln	810	6	3.4	214	2	Q7WAD1	Q7wad1 bordetella
738	3.4	196	2	Q9HZR6	Q9hzr6 pseudomonas	811	6	3.4	214	2	Q6PNC9	Q6pnc9 uncultured
739	3.4	197	1	VHR2_CAPVK	P19747 capripoxvir	812	6	3.4	216	2	Q6NCR4	Q6ncr4 homo sapien
740	3.4	197	2	Q6CB54	Q6cb54 yarrowia li	813	6	3.4	217	2	Q82GR6	Q82gr6 streptomyc
741	3.4	197	2	Q9VZP1	Q9vzp1 dirosophila	814	6	3.4	217	2	Q89BP9	Q89bp9 bradyrhizob
742	3.4	197	2	Q8Y7N2	Q8y7n2 listeria mo	815	6	3.4	217	2	Q89BP9	Q89bp9 bradyrhizob
743	3.4	197	2	Q92CG6	Q92cg6 listeria in	816	6	3.4	217	2	Q9X5C4	P46428 anophelies g
744	3.4	197	2	Q92T19	Q92t19 rhizobium m	817	6	3.4	218	1	GTS_ANOGA	Q9x5c4 streptococc
745	3.4	197	2	Q720I3	Q720i3 listeria mo	818	6	3.4	218	2	Q6PEG3	Q6peg3 homo sapien
746	3.4	197	2	Q8EMJ1	Q8emj1 mycoplasma	819	6	3.4	218	2	Q8LEB1	Q8leb1 arabidopsis
747	3.4	197	2	Q8KOK8	Q8kok8 mus musculu	820	6	3.4	218	2	Q93XZ7	Q93xz7 arabidopsis
748	3.4	197	2	Q8UTU1	Q8utu1 lumpy skin	821	6	3.4	218	2	Q8ID53	Q8id53 bacillus ce
749	3.4	197	2	Q8JU06	Q8ju06 lumpy skin	822	6	3.4	218	2	Q6HGF1	Q6hgf1 bacillus th
750	3.4	197	2	Q7THD0	Q7thd0 capripoxvir	823	6	3.4	219	2	Q635P2	Q635p2 bacillus ce
751	3.4	198	1	P8T2_YEAST	Q12335 saccharomyc	824	6	3.4	219	2	Q731R1	Q731r1 bacillus ce
752	3.4	198	1	VHR2_LSDV	Q91mu3 lumpy skin	825	6	3.4	219	2	Q81MU1	Q81m1 bacillus an
753	3.4	198	2	Q6FM13	Q6fm13 candida gla	826	6	3.4	219	2	Q89Z24	Q89z24 bacteroides
754	3.4	198	2	Q857J9	Q857j9 mycobacteri	827	6	3.4	219	2	Q6HEC8	Q6hec8 bacillus th
755	3.4	198	2	Q7FS93	Q7fs93 sorghum bic	828	6	3.4	220	1	YF09_HELPJ	Q9z6j9 helicobacte
756	3.4	198	2	Q8YNH6	Q8ynh6 anabaena sp	829	6	3.4	220	1	YF09_HELPJ	Q9z6j9 helicobacte
757	3.4	198	2	Q89B11	Q89b11 bradyrhizob	830	6	3.4	220	2	Q7QDT1	Q7qdt1 oryza sativ
758	3.4	199	2	Q6MOP6	Q6mof6 mechanococ	831	6	3.4	220	2	Q7XJ12	Q7xj12 leptospiril
759	3.4	199	2	Q9W8S1	Q9w8s1 arabidopsis	832	6	3.4	220	2	Q7X1N0	Q7x1n0 agrobacteri
760	3.4	199	2	Q8XHN9	Q8xhn9 clostridium	833	6	3.4	220	2	Q9F5G6	Q9f5g6 agrobacteri
761	3.4	199	2	Q6N4G9	Q6n4g9 rhodopseudo	834	6	3.4	220	2	Q92QW3	Q92qw3 rhizobium m



835	6	3.4	220	2	Q72H14	Q72h14 thermus the	908	6	3.4	237	2	Q651C1	Q651c1 oryza sativ
836	6	3.4	220	2	Q73MF5	Q73mf5 treponema d	909	6	3.4	237	2	Q7P6D4	Q7P6d4 fusobacteri
837	6	3.4	221	2	Q8E733	Q8e733 streptococc	910	6	3.4	237	2	Q9F0X5	Q9F0x5 pseudomonas
838	6	3.4	222	2	Q8IX38	Q8ix38 homo sapien	911	6	3.4	237	2	Q8KH02	Q8KH02 mus musculu
839	6	3.4	222	2	Q9G9D8	Q9g9d8 ascaphus tr	912	6	3.4	238	2	Q6CVA4	Q6Cva4 kluyveromyc
840	6	3.4	223	2	Q7NSH4	Q7nsh4 chromobacte	913	6	3.4	238	2	Q7Z5X6	Q7Z5x6 homo sapien
841	6	3.4	223	2	Q9L218	Q9l218 streptomyce	914	6	3.4	238	2	Q9Z5W3	Q9Z5w3 pseudomonas
842	6	3.4	224	2	Q7OD44	Q7oda4 saccharomyc	915	6	3.4	238	2	Q67863	Q67863 aquifex ae
843	6	3.4	224	2	Q7OD47	Q7oda7 saccharomyc	916	6	3.4	238	2	Q61NV3	Q61nv3 xenopus lae
844	6	3.4	224	2	Q7ODB2	Q7odb2 saccharomyc	917	6	3.4	239	2	Q8MUJ2	Q8muJ2 homo sapien
845	6	3.4	224	2	Q8YA47	Q8ya47 listeria mo	918	6	3.4	239	2	Q9X5C5	Q9X5c5 streptococc
846	6	3.4	224	2	Q9ZEW8	Q9zew8 listeria in	919	6	3.4	239	2	Q9ZJ44	Q9Zj44 rhizobium m
847	6	3.4	224	2	Q97FM6	Q97fm6 clostridium	920	6	3.4	239	2	Q6ST87	Q6ste87 cereal yell
848	6	3.4	224	2	Q72322	Q72322 listeria mo	921	6	3.4	240	2	Q9EDY3	Q9edy3 homo sapien
849	6	3.4	225	2	Q9E6H5	Q9e6h5 homo sapien	922	6	3.4	240	2	Q9SZC9	Q9szc9 homo sapien
850	6	3.4	226	1	YCKA_BACSU	P42399 bacillus su	923	6	3.4	240	2	Q9V402	Q9v402 drosophila
851	6	3.4	227	1	COX2_BACSU	P38596 halichoerus	924	6	3.4	240	2	Q8VTU0	Q8vtu0 listeria mo
852	6	3.4	227	1	COX2_HAIRGR	000528 phoca vitul	925	6	3.4	240	2	Q6M1L1	Q6m1l1 bdellovibri
853	6	3.4	227	1	Q679G9	Q679g9 muscela vis	926	6	3.4	240	2	Q6NDW9	Q6ndw9 rhodospseud
854	6	3.4	227	2	Q679H0	Q679h0 guilo guilo	927	6	3.4	240	2	Q71MS7	Q71ms7 listeria mo
855	6	3.4	227	2	Q679H4	Q679h4 phoca largh	928	6	3.4	240	2	Q90WT2	Q90wt2 brachydantio
856	6	3.4	227	2	Q679H5	Q679h5 phoca hisp	929	6	3.4	240	2	Q61QV5	Q61qv5 brachydantio
857	6	3.4	227	2	Q679H6	Q679h6 phoca groen	930	6	3.4	241	2	Q6LKY0	Q6lky0 photobacter
858	6	3.4	227	2	Q679H7	Q679h7 cystophora	931	6	3.4	241	2	Q7V7E3	Q7v7e3 prochloroco
859	6	3.4	227	2	Q679H8	Q679h8 erignathus	932	6	3.4	241	2	Q8Z6R4	Q8z6r4 streptomyce
860	6	3.4	227	2	Q679H9	Q679h9 monachus mo	933	6	3.4	241	2	Q89C05	Q89c05 bradyrhizob
861	6	3.4	227	2	Q679I0	Q679i0 monachus sc	934	6	3.4	242	1	FLIG_SHIBO	FLIG_SHIBO
862	6	3.4	227	2	Q679I1	Q679i1 mirounga le	935	6	3.4	242	1	Q9G9D7	Q9g9d7 ascaphus tr
863	6	3.4	227	2	Q679I5	Q679i5 leptonychot	936	6	3.4	242	2	Q40670	Q40670 oryza sativ
864	6	3.4	227	2	Q679I6	Q679i6 hydrurga le	937	6	3.4	242	2	Q8C658	Q8c658 mus musculu
865	6	3.4	227	2	Q679J0	Q679j0 ommatophoca	938	6	3.4	243	1	Q8C658	P30712 homo sapien
866	6	3.4	227	2	Q679J0	Q679j0 jobodon car	939	6	3.4	244	2	Q65ZC8	Q65zc8 homo sapien
867	6	3.4	227	2	Q9LHX1	Q9lhx1 oryza sativ	940	6	3.4	244	2	Q61B75	Q61b75 homo sapien
868	6	3.4	227	2	Q8RPE9	Q8rpe9 legionella	941	6	3.4	245	1	T2M4_METJA	T2M4_METJA
869	6	3.4	227	2	Q65NM3	Q65nm3 bacillus th	942	6	3.4	245	2	Q8ZMB3	Q8zmb3 pyrobaculum
870	6	3.4	227	2	Q9PMJ9	Q9pmj9 campylobact	943	6	3.4	245	2	Q6CAL5	Q6cal5 giardia lam
871	6	3.4	227	2	Q9YGT6	Q9ygt6 brachydantio	944	6	3.4	245	2	Q7QZ93	Q7qz93 yarrowia li
872	6	3.4	228	1	PCAI_ACTIAD	Q43973 acetobact	945	6	3.4	245	2	Q95LW2	Q95lw2 maceca faec
873	6	3.4	228	2	Q52047	Q52047 plasmid phv	946	6	3.4	245	2	Q30366	Q30366 alcaligenes
874	6	3.4	228	2	Q29279	Q29279 archaeoglob	947	6	3.4	245	2	Q8P0G8	Q8p0g8 streptococc
875	6	3.4	228	2	Q7QDM6	Q7qdm6 anopheles g	948	6	3.4	245	2	Q8YEL9	Q8yel9 bruceella me
876	6	3.4	228	2	Q679I2	Q679i2 mirounga an	949	6	3.4	245	2	Q8G364	Q8g364 bruceella su
877	6	3.4	228	2	Q7QAY5	Q7qay5 anopheles g	950	6	3.4	245	2	Q9KCT0	Q9kct0 rhizobium m
878	6	3.4	229	2	Q8DSQ2	Q8dsq2 streptococc	951	6	3.4	245	2	Q8UGB3	Q8ugb3 agrobacteri
879	6	3.4	229	2	Q8FBL7	Q8fbl7 escherichia	952	6	3.4	245	2	Q8UIY1	Q8uiy1 agrobacteri
880	6	3.4	229	2	Q91W91	Q91w91 mus musculu	953	6	3.4	246	1	NODG_AZOB	NODG_AZOB
881	6	3.4	230	1	RECK_AGRTS	Q8ub72 agrobacteri	954	6	3.4	246	2	Q9N4A0	Q9n4a0 caenorhabdi
882	6	3.4	230	2	Q6ICJ4	Q6icj4 homo sapien	955	6	3.4	246	2	Q9U4U4	Q9u4u4 cryptospori
883	6	3.4	230	2	Q6JHR1	Q6jhr1 saccharopol	956	6	3.4	246	2	Q7WAI5	Q7wai5 bordetella
884	6	3.4	230	2	Q7MH80	Q7mh80 vibrio vuln	957	6	3.4	246	2	Q7WJN2	Q7wjn2 bordetella
885	6	3.4	230	2	Q7NJJ0	Q7njj0 gloeobacter	958	6	3.4	246	2	Q8A2912	Q8a2912 streptomyce
886	6	3.4	231	2	Q86OK1	Q86ok1 adinetia vag	959	6	3.4	246	2	Q8DA72	Q8da72 vibrio vuln
887	6	3.4	231	2	Q93W48	Q93w48 bacillus th	960	6	3.4	247	2	Q6O0X0	Q6oqx0 shigella bo
888	6	3.4	231	2	Q89E35	Q89e35 bradyrhizob	961	6	3.4	247	2	Q65U71	Q65u71 manihelma
889	6	3.4	232	2	Q6YWY3	Q6ywy3 oryza sativ	962	6	3.4	249	2	Q8KL79	Q8kl79 rhizobium e
890	6	3.4	232	2	Q8PMM2	Q8pmm2 xanthomonas	963	6	3.4	250	1	WSE2_HUMAN	WSE2_HUMAN
891	6	3.4	233	1	RPE_CHLTR	Q84123 chlamydia t	964	6	3.4	250	1	Y0E2_PHOIL	Y0E2_PHOIL
892	6	3.4	233	2	Q12I31	Q12i31 cloning vec	965	6	3.4	250	2	Q9P9C3	Q9p9c3 uncultured
893	6	3.4	233	2	Q8IX39	Q8ix39 homo sapien	966	6	3.4	250	2	Q17154	Q17154 caenorhabdi
894	6	3.4	233	2	Q7W6H4	Q7w6h4 wolinnella s	967	6	3.4	250	2	Q6B355	Q6b355 uncultured
895	6	3.4	233	2	Q893J4	Q893j4 clostridium	968	6	3.4	250	2	Q9KKES	Q9kkes corynebacte
896	6	3.4	234	2	Q7NZN8	Q7nzn8 chromobacte	969	6	3.4	250	2	Q81174	Q81174 bacillus ce
897	6	3.4	234	2	Q8ZMP8	Q8zmp8 streptomyce	970	6	3.4	250	2	Q6ALJ9	Q6alaj9 bradyrhizob
898	6	3.4	234	2	Q8ZSP8	Q8zsp8 nitrospirone	971	6	3.4	250	2	Q6ALJ9	Q6alaj9 bacillus th
899	6	3.4	234	2	Q8EMT5	Q8emt5 mycoplasma	972	6	3.4	251	2	Q6HC40	Q6hc40 bacillus th
900	6	3.4	235	2	Q8I7B9	Q8i7b9 echinococcu	973	6	3.4	251	2	Q8S2R9	Q8s2r9 theilungiel
901	6	3.4	235	2	Q8R0A6	Q8r0a6 mus musculu	974	6	3.4	251	2	Q8R846	Q8r846 xanthomonas
902	6	3.4	235	2	Q921F5	Q921f5 mus musculu	975	6	3.4	252	2	Q9FH68	Q9fh68 arabidopsis
903	6	3.4	235	2	Q6GLA0	Q6glao xenopus tro	976	6	3.4	252	2	Q6LTC3	Q6ltc3 photobacter
904	6	3.4	236	2	Q7RNS7	Q7rns7 plasmodium	977	6	3.4	252	2	Q7TUI1	Q7tui1 rhodospirell
905	6	3.4	236	2	Q9VZ10	Q9vz10 diosiphilla	978	6	3.4	252	2	Q9K825	Q9k825 bacillus ha
906	6	3.4	236	2	Q8Y4B5	Q8y4b5 listeria mo	979	6	3.4	252	2	Q9KRM9	Q9krm9 bacillus ha
907	6	3.4	236	2	Q927Z2	Q927z2 listeria in	980	6	3.4	252	2		

981 6 3.4 253 2 Q6CFY6 Q6CFY6 yarrowia 11  
 982 6 3.4 253 2 Q6F9R6 Q6F9R6 actinobact  
 983 6 3.4 253 2 Q89CF1 Q89CF1 bradyrhizob  
 984 6 3.4 254 2 Q8NDT5 Q8NDT5 homo sapien  
 985 6 3.4 254 2 Q95XU1 Q95XU1 caenorhabdi  
 986 6 3.4 254 2 Q9V3R0 Q9V3R0 drosophila  
 987 6 3.4 254 2 Q632B0 Q632B0 bacillus ce  
 988 6 3.4 254 2 Q72YCS Q72YCS bacillus ce  
 989 6 3.4 254 2 Q816A9 Q816A9 bacillus ce  
 990 6 3.4 254 2 Q81XP1 Q81XP1 bacillus an  
 991 6 3.4 254 2 Q6HB08 Q6HB08 bacillus th  
 992 6 3.4 254 2 Q8QNB1 Q8QNB1 ectocarpus  
 993 6 3.4 255 2 Q81BQ1 Q81BQ1 plasmodium  
 994 6 3.4 255 2 Q8RL62 Q8RL62 pseudomonas  
 995 6 3.4 255 2 Q929Y8 Q929Y8 actinobacil  
 996 6 3.4 255 2 Q8BCX9 Q8BCX9 xanthomonas  
 997 6 3.4 255 2 Q8BPB7 Q8BPB7 xanthomonas  
 998 6 3.4 255 2 Q61QH2 Q61QH2 brachydanio  
 999 6 3.4 256 2 Q8TTL5 Q8TTL5 mechanosarc  
 1000 6 3.4 256 2 Q8ZRR8 Q8ZRR8 salmoneilla

## ALIGNMENTS

RESULT 1  
 IL20\_HUMAN STANDARD; PRT; 176 AA.  
 ID Q9NYT1, Q96QZ6; (Rel. 41, Created)  
 AC 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 29-MAR-2004 (Rel. 43, Last annotation update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10)  
 DE (UN0857/PRO1861).  
 GN Name=IL20;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 OK [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2109717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;  
 RA Blumberg P., Conklin D., Xu W.F., Grossmann A., Brendler T.,  
 RA Carullo S., Egan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,  
 RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,  
 RA Prunkard D., Saxon S., Sprecher C., Maggic K., West J.,  
 RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;  
 RA "Interleukin 20: discovery, receptor identification, and role in  
 RA epidermal function."  
 RT Cell 104:9-19(2001).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Riederer M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RA "SealtSNPs. NHLBI HL6682 program for genomic applications, UW-  
 RA FHCC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Adaya B., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel P.,  
 RA Bacon D., Foster J., Grimaldi C., Gu Q., Haas P.E., Helms S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robble B., Sanchez C., Schoenfeld J.,  
 RA Seisagiri S., Stimmone L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vanden R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yanura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;  
 RA "The secreted protein discovery initiative (SPDI), a large-scale  
 RA effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment."  
 RT Genome Res. 13:2265-2270(2003).

RN [4]  
 RP SEQUENCE OF 25-39.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites."  
 RL Protein Sci. 13:2819-2824(2004).  
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and  
 CC peristalsis. Acts through STAT3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,  
 CC and other tissues.  
 CC -1- SIMILARITY: Belongs to the IL-10 family.  
 CC -----  
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DR EMBL; AF224266; AAF6679.1; -;  
 DR EMBL; AF402002; AAK8423.1; -;  
 DR EMBL; AY358320; AAQ8686.1; -;  
 DR HSSP; Q9UHD0; 1N1F.  
 DR Genew; HGNC:6002; IL20.  
 DR MIM; 605619; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0045517; F:Interleukin-20 receptor binding; TAS.  
 DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. . . ; TAS.  
 DR GO; GO:0045618; P:positive regulation of keratinocyte diffe. . . ; TAS.  
 DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. . . ; TAS.  
 DR GO; GO:0050727; P:regulation of inflammatory response; TAS.  
 DR InterPro; IPR000098; Interleukin\_10.  
 DR ProDom; PD003687; Interleukin\_10; 1.  
 DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
 DR KW Cytokine; Direct protein sequencing; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 176 Interleukin-20.  
 FT DISULFID 33 126 Potential.  
 FT DISULFID 80 132 Potential.  
 FT DISULFID 81 134 Potential.  
 FT CONFLICT 48 48 E -> D (in Ref. 1).  
 FT CONFLICT 126 126 C -> S (in Ref. 3).  
 SQ SEQUENCE 176 AA; 20072 MM; 838599250B6C447 CNG64;  
 Query Match 72.7%; Score 128; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-125;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 49 IRGSVQAKDGNIDIRILRTSTLDDTPKRNCCILRLRLYLDRVFNKYOTPDHYTLRK 108  
 DB 49 IRGSVQAKDGNIDIRILRTSTLDDTPKRNCCILRLRLYLDRVFNKYOTPDHYTLRK 108  
 QY 109 ISSLSANSLTTRKDLRLCHAMTCHCGEANKTSQILSHFEKLEPQAAVVKALGELDIL 168  
 DB 109 ISSLSANSLTTRKDLRLCHAMTCHCGEANKTSQILSHFEKLEPQAAVVKALGELDIL 168  
 QY 169 LQNMETE 176  
 DB 169 LQNMETE 176  
 RESULT 2  
 IL20\_MOUSE STANDARD; PRT; 176 AA.  
 ID Q9KVV9;  
 AC 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).  
 GN Name=IL20;

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA MEDLINE=21097717; PubMed=11163336; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brendler T.,
RA Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jelnick L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Maggie K., West J.,
RA Whitmore T.E., Yao L., Knechle M.K., Dale B.A., Chandrasekhar Y.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC psoriasis. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AF224267; AAF36680.1; -.
DR HSSP; Q9UHD0; INIF.
DR MGD; MG1:1890473; I120.
DR GO; GO:004517; F:interleukin-20 receptor binding; IPI.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR DR Cytokine; sigmal.
KW SIGNAL.
FT CHAIN 1 24 Potential.
FT DISULFID 33 126 Interleukin-20.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
SQ SEQUENCE 176 AA; 20097 MW; 08577AF6565771 CRC64;

Query Match 7.4%; Score 13; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TLKRISLANSFL 117
Db 105 TLKRISLANSFL 117

RESULT 3
06L2K4 PRELIMINARY; PRT; 137 AA.
AC 06L2K4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical membrane spanning protein.
GN OrderedLocuNames=PT00213;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fletterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,

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RA Schepers B., Dock C., Antranikian G., Liebl M.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AB017261; AAT42798.1; -.
KW Complete proteome; Hypochemical protein.
SQ SEQUENCE 137 AA; 16535 MW; DD2928CD82E98D01 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LSARFYL 18
Db 46 LSARFYL 53

RESULT 4
SURE_PSEPK STANDARD; PRT; 249 AA.
ID SURE_PSEPK
AC Q8BMF1;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid phosphatase sure (EC 3.1.3.2).
GN Name=sure; OrderedLocuNames=PP1620;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beaman M.C., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouf H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzez A., Utechtack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Medler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Helm S.,
RA Kiewitz C., Elsen J.A., Timmls K.N., Duesterhoeft A., Tuenmler B.,
RA Praser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
CC phosphate.
CC -1- Cofactor: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the sure acid phosphatase family.
CC -----
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CC -----
DR EMBL; AB016780; AAM67241.1; -.
DR HSSP; P96112; IJ9L.
DR TIGR; PP1620; -.
DR HAMAP; MF_00060; -; 1.
DR InterPro; IPR002828; SURE.
DR Pfam; PF01975; SURE; 1.
DR ProDom; PD005378; SURE; 1.
KW Complete proteome; Hydrolyase; Magnesium.
FT ACT SITE 123
FT METAL 8 123 Potential.
FT METAL 9 9 Magnesium (By similarity).
FT METAL 39 39 Magnesium (By similarity).
FT METAL 91 91 Magnesium (By similarity).
SQ SEQUENCE 249 AA; 26317 MW; 824P1D5F7C8B8073 CRC64;

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Query Match 4.5%; Score 8; DB 1; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAFSLLS 12  
 |||||  
 Db 119 SLAFSLLS 126

## RESULT 5

Q9KDB7 PRELIMINARY; PRT; 279 AA.  
 AC Q9KDB7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE BH1296 protein.  
 GN OrderedLocustNames=BH1296;  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125;  
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL, AP001511; BAB05015.1; -.  
 DR PIR; H83811; H83811.  
 KW Complete proteome.  
 SQ SEQUENCE 279 AA; 32457 MM; D92AE286356C30D5 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFSLISA 13  
 |||||  
 Db 13 LAFSLISA 20

## RESULT 6

Q8UIB8 PRELIMINARY; PRT; 305 AA.  
 AC Q8UIB8; Q7D1K4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein Atu0379 (AGR\_C\_664p).  
 GN OrderedLocustNames=AGR\_C\_664; Atu0379;  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dupont;  
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;  
 RA Wood D.W., Seubert J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutyavina T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323(2001).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Cereoni;  
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Urrutia B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L.,  
 RA Houtrel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,  
 RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
 RA Fiebo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL, AE009009; AAL41401.1; -.  
 DR EMBL, AE007975; AAK6196.1; -.  
 DR PIR; C97405; C97405.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 305 AA; 32574 MM; A2A4683FD67AEFF0 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 QAAVVKAL 162  
 |||||  
 Db 256 QAAVVKAL 263

## RESULT 7

Q82S35 PRELIMINARY; PRT; 396 AA.  
 AC Q82S35;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Restriction modification system, type I (EC 3.1.21.3).  
 GN OrderedLocustNames=NE2526;  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RX DOI=10.1128/JB.185.9.2759-2773.2003;  
 RA Chain P., Lamerdin J.B., Larimer F.W., Regala W., Lao V., Land M.L.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
 RA Archiero D.M., Hommes N.G., Whitaker M.M., Arp D.J.,  
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea.";  
 RL J. Bacteriol. 185:2759-2773(2003).  
 DR EMBL, BX321865; CAD86438.1; -.  
 DR GO; GO:0003677; P:DNA binding; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0009035; F:Type I site-specific deoxyribonuclease actl. . .; IEA.  
 DR GO; GO:0006304; P:DNA modification; IEA.  
 DR InterPro; IPR000055; Rest mod DNA.  
 DR Pfam; PF01420; Methylase S; 2.  
 KW Complete proteome; Hydrolase.  
 SQ SEQUENCE 396 AA; 43995 MM; 056FC6AB5DCA9DC CRC64;

Query Match 4.5%; Score 8; DB 2; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 SSLANSFL 117  
 |||||  
 Db 198 SSLANSFL 205

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RESULT 8
ANSP_STRCO
ID ANSP_STRCO STANDARD; PRT; 489 AA.
AC 09X7P0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE l-asparagine permease (l-asparagine transport protein).
GN Nameanap; OrderedLocustNames=SC06734; ORNames=SC57A.17;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12009553; DOI=10.1038/41741a1;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Godle A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Laire L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajadream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)".
RL Nature 417:141-147(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
CC superfamily. Amino acid transporter (AAT) (TC 2.A.3.1) family.
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DR DR EMBL: AL39129; CAB40684.1; -.
DR PIR: T35259; T35259.
DR InterPro: IPR002293; AA/permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR Pfam: PF00324; AA_permease; 1.
DR TIGRfam: TIGR01773; GABaperm; 1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
KW Amino-acid transport; Complete proteome; Transmembrane; Transport.
FT TRANSMEM 38 58 Potential.
FT TRANSMEM 62 82 Potential.
FT TRANSMEM 113 133 Potential.
FT TRANSMEM 150 170 Potential.
FT TRANSMEM 175 195 Potential.
FT TRANSMEM 223 243 Potential.
FT TRANSMEM 268 288 Potential.
FT TRANSMEM 302 322 Potential.
FT TRANSMEM 357 377 Potential.
FT TRANSMEM 382 402 Potential.
FT TRANSMEM 426 446 Potential.
FT TRANSMEM 452 472 Potential.
SQ SEQUENCE 489 AA; 51797 MW; 219F74312E81F14C CRC64;

Query Match 4.5%; Score 8; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 158 VVKALGEL 165
DB 81 VVKALGEL 88

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RESULT 9
MURE_BIFLO
ID MURE_BIFLO STANDARD; PRT; 517 AA.
AC 08G4M3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-N-acetylmuuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNac-tripeptide synthetase).
GN Name=mure; OrderedLocustNames=BL1356;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteriales; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxId=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RC MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snell B., Villanova D., Berger B.,
RA Pessi G., Zwalten M.-C., Desiere F., Bork P., Delley M.,
RA Primrose R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RT Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminopimelate = ADP + phosphate + UDP-
CC N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diamino-
CC heptanedioate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the mureD family.
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CC -----
DR DR EMBL: AE014765; AAN25156.1; -.
DR HAMAP: MF_00208; -.
DR InterPro: IPR004101; Mur_ligase_C.
DR InterPro: IPR000713; Mur_ligase_N.
DR Pfam: PF01225; Mur_ligase; 1.
DR Pfam: PF02875; Mur_ligase_C; 1.
KW ATP-binding; Cell division; Cell wall; Complete proteome; Ligase;
KW Peptidoglycan synthesis.
FT NP_BIND 125 131s ATP (Potential).
SQ SEQUENCE 517 AA; 56338 MW; 87F39226FDD05940F CRC64;

Query Match 4.5%; Score 8; DB 1; Length 517;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 9 SLISAAFY 16
DB 104 SLISAAFY 111

RESULT 10
Q7ZVG0
ID Q7ZVG0 PRELIMINARY; PRT; 531 AA.
AC Q7ZVG0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Regulator of chromosome condensation (RCC1) and BTB (POZ) domain

```

DE containing protein 1.  
 GN ORFNames=zgc:56037;  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OK Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 [1]  
 RN STRAIN=AB; TISSUE=whole body;  
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Fellous B.A., Groves L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner I., Shennan C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stabileon M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange T.E.,  
 RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettlemen M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=AB; TISSUE=whole body;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC045877; AAH45877.1; -.  
 DR HSSP; O87916; IJTD.  
 DR ZFIN; ZDB-GENE-030131-7951; zgc:56037.  
 DR GO; GO:0005515; P:protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_PZ.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR009091; RCT1/BLIP-II.  
 DR InterPro; IPR00408; Reg\_chromatins.  
 DR Pfam; PF00651; BTB; 2.  
 DR PRINTS; PR00633; RCDNSATON.  
 DR SMART; SM00225; BTB; 1.  
 DR PROSITE; PS50097; BTB; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00626; RCT1\_2; 2.  
 DR PROSITE; PS50012; RCT1\_3; 4.  
 DR SEQUENCE 531 AA; 58711 MW; D5D9C00ABB6A18D3 CRC64;  
 SO  
 Query Match 4.5%; Score 8; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 AFSLSAA 14  
 Db 472 AFSLSAA 479  
 RESULT 11  
 Q83BA7 PRELIMINARY; PRT; 698 AA.  
 AC Q83BA7;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 GN Membrane protein, putative.  
 OS OrderedLocustNames=CBU1605;  
 CC Coxiella burnetii.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

CC Coxiellaceae; Coxiella.  
 OK NCBI\_TaxID=777;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=2260857; PubMed=12704232; DOI=10.1073/pnas.0931379100;  
 RX Seeshadri R., Paulsen I.T., Eissen J.A., Read T.D., Nelson K.E.,  
 RA Nelson W.C., Ward N.L., Tetteilin H., Davidsen T.M., Beaman M.J.,  
 RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,  
 RA Khouiri H.M., Lee K.H., Carcy H.A., Scanlan D., Heinzen R.A.,  
 RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.,  
 RT "Complete genome sequence of the Q-fever pathogen, Coxiella  
 burnetii.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).  
 DR EMBL; AB016965; AAC91102.1; -.  
 DR TIGR; CBU1605; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR01066; MscC\_channel\_C.  
 DR InterPro; IPR00685; MscC\_channel.  
 DR InterPro; IPR01014; MscS\_transmembr.  
 DR InterPro; IPR010920; Sm\_like\_riboprot.  
 DR Pfam; PF00924; Msc\_channel; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 698 AA; 79951 MW; 3A5251E0A7FFDB5E CRC64;  
 SO  
 Query Match 4.5%; Score 8; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 SLSAFLSL 11  
 Db 650 SLSAFLSL 657  
 RESULT 12  
 P5CS\_LYCSES STANDARD; PRT; 717 AA.  
 AC 096480;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Delta 1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate  
 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK); Gamma-glutamyl  
 phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde  
 dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)].  
 GN Name=PRO2;  
 OS Lycopersicon esculentum (Tomato).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 CC Lamiales; Solanales; Solanaceae; Solanum.  
 OK NCBI\_TaxID=4081;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. Alisa Craig;  
 RA Hasegawa A., Garcia-Rios M., Fujita T., Bressan R.A., Joly R.S.,  
 RA Hasegawa M.P., Geonka L.N.;  
 RT "Cloning of tomato and tomato2 from Lycopersicon esculentum L.:  
 coexistence of polistronic and monocistronic genes which encode the  
 RT enzymes catalyzing the first two steps of proline biosynthesis.";  
 RL (er) Plant Gene Register PGR96-077.  
 CC -1- FUNCTION: P5CS plays a key role in proline biosynthesis, leading  
 to osmoregulation in plants.  
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-  
 phosphate.  
 CC -1- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate +  
 NADP(+) = L-glutamyl 5-phosphate + NADPH.  
 CC -1- ENZYME REGULATION: Feedback regulated by proline.  
 CC -1- PATHWAY: Proline biosynthesis; first step.  
 CC -1- PATHWAY: Proline biosynthesis; second step.  
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in leaves and is  
 inducible in roots subjected to salt stress.  
 CC -1- SIMILARITY: In the N-terminal section; belongs to the glutamate 5-  
 kinase family.



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CC -1- SIMILARITY: In the C-terminal section; belongs to the gamma-
CC glutamyl phosphate reductase family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC -----
DR EMBL; U60267; AAB67875.1; -.
DR PIR; T07422; T07422.
DR HSSP; Q9WYC9; 1020.
DR InterPro; IPR001048; Aa_kinase.
DR InterPro; IPR000965; GgInt_pp_reduct.
DR InterPro; IPR001057; Glu_5kinase.
DR InterPro; IPR005766; P5_carboxy_syn.
DR InterPro; IPR005715; Prob.
DR Pfam; PF00696; Aa_kinase; 1.
DR PRINTS; PR00474; GLUSKINASE.
DR TIGRfam; TIGR01092; P5CS; 1.
DR TIGRfam; TIGR00407; ProA; 1.
DR PROSITE; PS00902; GLUTAMATE_5_KINASE; 1.
DR PROSITE; PS01223; PROA; 1.
DR Kinase; Multifunctional enzyme; NADP; Oxidoreductase;
DR Proline biosynthesis; Transferrase.
DR DOMAIN 1 296 Glutamate 5-kinase.
DR DOMAIN 297 717 Gamma-glutamyl phosphate reductase.
DR SEQUENCE 717 AA; 77589 MW; 1E206428B69EEBCA CRC64;

Query Match 4.5%; Score 8; DB 1; Length 717;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 KISSLANS 115
DB 365 KISSLANS 372

RESULT 13
Q7MBR3 PRELIMINARY; PRT; 719 AA.
AC Q7MBR3;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DR Putative toxin secretion ABC transporter, ATP-binding subunit.
GN Ordered locus names=VVA1677;
OS Vibrio vulnificus (strain V1016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
[1]
RP SEQUENCE FROM N.A.
RA PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-T., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-D., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587(2003).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AP005351; BAC97703.1; -.
DR HSSP; P26361; 1R0W.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; IEA.
DR GO; GO:0008223; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR011527; ABC_membrane_1.

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DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005074; Peptidase_C39.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR PROSITE; PS00929; ABC_TM1F; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
DR SEQUENCE 719 AA; 80876 MW; 6144A6D1C0505A7 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LRRHLRL 89
DB 258 LRRHLRL 265

RESULT 14
Q8E874 PRELIMINARY; PRT; 725 AA.
AC Q8E874;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 26, Last annotation update)
DR Putative ABC transporter, ATP-binding subunit/permease protein,
DR putative.
GN Ordered locus names=SOA0049;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Bacteriia; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OX NCBI_TaxID=70863;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=NR-1;
RA MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Galois B.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Meele B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Dukin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impram M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khoult H.M., Gill J.,
RA Utechback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nelson K.H., Frazer C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AB015912; AAN5285.1; -.
DR HSSP; P08716; 1MT0.
DR MEROPS; C39.005; -.
DR TIGR; SOA0049; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR005074; Peptidase_C39.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.

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DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS50929; ABC\_TM1F; 1.  
 DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 725 AA; 80452 MW; 890B16CE3A6639B2 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 725;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LRRHLRL 89  
 |||||  
 DB 263 LRRHLRL 270

## RESULT 15

O9XGC4 PRELIMINARY; PRT; 762 AA.  
 AC O9XGC4;  
 DT 01-NOV-1999 (TRMBLrel. 12, Created)  
 DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)  
 DR Pyroline-5-carboxylate synthetase (EC 2.7.2.11).  
 GN Name=p5cs;  
 OS Vitis vinifera (Grape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Vitaceae; Vitis.  
 OC NCBI\_TaxID=29760;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Grape berry;  
 RX MEDLINE=99329329; PubMed=10398729; DOI=10.1104/pp.120.3.923;  
 RT Stines A.P., Naylor D.J., Hoj P.H., van Heeswijk R.;  
 RT "Proline accumulation in developing grapevine fruit occurs  
 RT independently of changes in the levels of delta1-pyrolone-5-  
 RT carboxylate synthetase mRNA or protein.";  
 RL Plant Physiol. 120:923-923 (1999).  
 DR EMBL; AJ005686; CAB40834.1; -.  
 DR HSR; O9MYC9; 1020.  
 DR GO; GO:0005737; Cytoplasm; IEA.  
 DR GO; GO:0004349; F:glutamate 5-kinase activity; IEA.  
 DR GO; GO:0004350; F:glutamate-5-semialdehyde dehydrogenase acti. .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008652; P:amino acid biosynthesis; IEA.  
 DR GO; GO:000561; P:pyroline biosynthesis; IEA.  
 DR InterPro; IPR01048; Aa\_Kinase.  
 DR InterPro; IPR000965; Gglut\_pp\_reduct.  
 DR InterPro; IPR01057; Glu\_5Kinase.  
 DR InterPro; IPR005766; P5\_Carboxy\_syn.  
 DR InterPro; IPR005715; ProB.  
 DR Pfam; PF00696; Aa\_Kinase; 1.  
 DR PRINTS; PIRSF036429; P5C\_syn; 1.  
 DR PRINTS; PRO0474; GLU5KINASE.  
 DR TIGRfams; TIGR01092; P5CS; 1.  
 DR TIGRfams; TIGR00407; proA; 1.  
 DR TIGRfams; TIGR01027; proB; 1.  
 KW transferase.  
 SQ SEQUENCE 762 AA; 82682 MW; 586A3A48FC8A1C CRC64;

Query Match 4.5%; Score 8; DB 2; Length 762;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 KISSLANS 115  
 |||||  
 DB 367 KISSLANS 374

Search completed: November 2, 2005, 19:01:38  
 Job time : 236 secs



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OM protein - protein search, using sw model

Run on: November 2, 2005, 18:51:12 / Search time 39 Seconds  
(without alignments)  
434.209 Million cell updates/sec

Title: US-10-748-484-2

Sequence: 1 MKASLSAFSLSAFYLLMT.....AVKALGIDLILQNMETE 176

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 860

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	4.5	279	2 H83811	hypothetical prote
2	8	4.5	305	2 AC2623	conserved hypotet
3	8	4.5	305	2 C97405	hypothetical prote
4	8	4.5	489	2 T35259	probable L-asparag
5	8	4.5	717	2 T07422	delta 1-pyrroline-
6	7	4.0	201	2 A47096	response regulator
7	7	4.0	213	2 G84828	hypothetical prote
8	7	4.0	217	2 JC5710	TBP-1 interacting
9	7	4.0	224	2 G70851	probable gid prote
10	7	4.0	241	2 C75329	conserved hypotet
11	7	4.0	251	2 T24485	hypothetical prote
12	7	4.0	260	2 T32329	hypothetical prote
13	7	4.0	293	2 E71674	hypothetical prote
14	7	4.0	327	2 A70392	UDP-glucose-4-epim
15	7	4.0	354	2 T04262	mitogen-activated
16	7	4.0	382	2 S63638	ubiquitinol-cytochro
17	7	4.0	388	2 A47032	galactokinase galk
18	7	4.0	389	2 S36638	glycoprotein Epi -
19	7	4.0	426	1 B69656	multidrug-efflux t
20	7	4.0	441	2 F71482	hypothetical prote
21	7	4.0	444	2 F96838	hypothetical prote
22	7	4.0	445	2 B86160	F22D16.4 protein -
23	7	4.0	471	2 T19147	hypothetical protei
24	7	4.0	473	2 T41500	hypothetical prote
25	7	4.0	478	2 C95981	probable membrane
26	7	4.0	480	2 T00971	NAD(P) transhydrog
27	7	4.0	512	2 D82444	probable transport
28	7	4.0	628	2 T38034	ATP synthase, Chai
29	7	4.0	649	2 C81687	

30	7	4.0	706	2 P86143	hypothetical prote
31	7	4.0	754	2 T00393	Nitrogen breakage
32	7	4.0	761	2 T05299	hypothetical prote
33	7	4.0	762	2 E64597	DNA mismatch repai
34	7	4.0	762	2 H71916	hypothetical prote
35	7	4.0	915	2 H96709	two-component regu
36	7	4.0	930	2 AG0410	hypothetical prote
37	7	4.0	1100	2 T47940	hypothetical prote
38	7	4.0	2165	2 T21371	hypothetical prote
39	7	4.0	4563	1 LPHUB	apolipoprotein B-1
40	7	3.4	54	2 H31445	ovomucoid, chird d
41	6	3.4	54	2 F61494	ovomucoid, chird d
42	6	3.4	54	2 F31447	ovomucoid, chird d
43	6	3.4	55	2 AF2035	hypothetical prote
44	6	3.4	56	2 A69837	hypothetical prote
45	6	3.4	62	2 D59103	hypothetical prote
46	6	3.4	63	2 S00951	hypothetical prote
47	6	3.4	66	2 D72607	hypothetical prote
48	6	3.4	69	2 F90476	probable membrane
49	6	3.4	70	2 AH1043	conserved hypotet
50	6	3.4	71	2 A10691	modulating protein
51	6	3.4	71	2 B85769	modulating protein
52	6	3.4	71	2 C64919	modulating protein
53	6	3.4	71	2 F90920	hypothetical prote
54	6	3.4	71	2 F81897	hypothetical prote
55	6	3.4	71	2 B63337	hypothetical prote
56	6	3.4	76	2 D81094	hypothetical prote
57	6	3.4	76	2 S74780	hypothetical prote
58	6	3.4	76	2 AG2612	hypothetical prote
59	6	3.4	80	2 B38908	hypothetical prote
60	6	3.4	81	2 C49029	T-cell receptor V
61	6	3.4	81	2 T03707	Reverse transcript
62	6	3.4	84	2 T11970	Photosystem I reac
63	6	3.4	86	2 AB0153	probable bacteriop
64	6	3.4	88	2 A90048	conserved hypotet
65	6	3.4	89	2 I51423	gonadoliberin prec
66	6	3.4	89	2 AP3590	hypothetical prote
67	6	3.4	92	2 S36498	E7 protein - human
68	6	3.4	92	2 T03665	reverse transcript
69	6	3.4	92	2 T03617	retrovirus-related
70	6	3.4	95	2 I46684	blaetocyst protei
71	6	3.4	100	2 F84766	hypothetical prote
72	6	3.4	114	2 B97638	gace2 (MJ223604) [
73	6	3.4	114	2 AF2861	quaternary ammoniu
74	6	3.4	115	2 H83430	type III export pr
75	6	3.4	117	2 E72732	hypothetical prote
76	6	3.4	117	2 A82495	conserved hypotet
77	6	3.4	117	2 AG2077	hypothetical prote
78	6	3.4	118	2 H72644	probable arabinoga
79	6	3.4	122	2 B86570	l14 ribosomal prot
80	6	3.4	122	2 G72054	ribosomal protein
81	6	3.4	122	2 E81664	ribosomal protein
82	6	3.4	122	2 D42645	conserved hypotet
83	6	3.4	122	2 C64422	conserved hypotet
84	6	3.4	123	2 A83432	probable membrane
85	6	3.4	124	2 S45788	hypothetical prote
86	6	3.4	126	2 B82690	translation initia
87	6	3.4	127	2 A97056	conserved hypotet
88	6	3.4	127	2 B89862	hypothetical prote
89	6	3.4	127	2 AD2636	En/Spm-like transp
90	6	3.4	127	2 C84502	hypothetical prote
91	6	3.4	129	2 F70670	hypothetical prote
92	6	3.4	133	2 A72675	hypothetical prote
93	6	3.4	139	2 A70881	hypothetical prote
94	6	3.4	141	2 F38164	hypothetical prote
95	6	3.4	141	2 A83178	hypothetical prote
96	6	3.4	141	2 F69392	probable CDP-alcoh
97	6	3.4	141	2 G72661	hypothetical prote
98	6	3.4	142	1 HAGY	hemoglobin alpha c
99	6	3.4	143	2 H71970	hypothetical prote
100	6	3.4	145	2 AE2962	conserved hypotet
101	6	3.4	145	2 E88462	protein C05H8.2 [1
102	6	3.4	151	2 A96493	hypothetical prote

hypothetical prote  
Nijmegen breakage  
hypothetical prote  
DNA mismatch repai  
hypothetical prote  
two-component regu  
hypothetical prote  
hypothetical prote  
apolipoprotein B-1  
ovomucoid, chird d  
ovomucoid, chird d  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable membrane  
conserved hypotet  
modulating protein  
modulating protein  
modulating protein  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
T-cell receptor V  
Reverse transcript  
Photosystem I reac  
probable bacteriop  
conserved hypotet  
gonadoliberin prec  
hypothetical prote  
E7 protein - human  
reverse transcript  
retrovirus-related  
blaetocyst protei  
hypothetical prote  
gace2 (MJ223604) [  
quaternary ammoniu  
type III export pr  
hypothetical prote  
conserved hypotet  
hypothetical prote  
probable arabinoga  
l14 ribosomal prot  
ribosomal protein  
ribosomal protein  
conserved hypotet  
conserved hypotet  
probable membrane  
hypothetical prote  
translation initia  
conserved hypotet  
hypothetical prote  
En/Spm-like transp  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable CDP-alcoh  
hypothetical prote  
hemoglobin alpha c  
hypothetical prote  
conserved hypotet  
protein C05H8.2 [1  
hypothetical prote

103	6	3.4	152	2	D97462	hypothetical prote	176	6	3.4	226	2	C69760	amino acid ABC tra
104	6	3.4	152	2	AE2680	transcription regu	177	6	3.4	227	2	S41838	cytochrome-c oxida
105	6	3.4	153	2	B47748	trans-regulatory s	178	6	3.4	227	2	S26154	cytochrome-c oxida
106	6	3.4	153	2	G65426	riboflavin synthas	179	6	3.4	227	2	D81292	probable DNA methy
107	6	3.4	153	2	E87313	conserved hypothet	180	6	3.4	228	1	A44570	3-oxoadipate CoA-c
108	6	3.4	154	2	AE7354	translational initia	181	6	3.4	228	2	G69372	hypothetical prote
109	6	3.4	157	2	B64529	probable signal pe	182	6	3.4	230	2	E98234	hypothetical prote
110	6	3.4	158	2	T46080	hypothetical prote	183	6	3.4	233	2	E71553	probable ribulose-
111	6	3.4	159	1	MMVZM1	T3A protein - shes	184	6	3.4	236	2	AE1387	two-component resp
112	6	3.4	159	2	T06899	hypothetical prote	185	6	3.4	236	2	AG1762	two-component resp
113	6	3.4	159	2	AB2051	hypothetical prote	186	6	3.4	238	2	C70479	thiol-dienulfide in
114	6	3.4	160	2	S00714	phycocyanin 1 alph	187	6	3.4	239	2	C95323	conserved hypothet
115	6	3.4	160	2	AB3559	transcription regu	188	6	3.4	242	2	S49462	cyclin - rice
116	6	3.4	161	2	H96966	penicillin importe	189	6	3.4	244	2	A56847	glutathione transf
117	6	3.4	162	2	S05712	phycocyanin 3 alph	190	6	3.4	245	2	D97493	3-oxoacyl-(acyl) ca
118	6	3.4	163	2	C71977	probable signal pe	191	6	3.4	245	2	AE2711	3-oxoacyl-(acyl) ca
119	6	3.4	164	2	T31280	benzoate 1,2-dioxy	192	6	3.4	245	2	AE3484	integral membrane
120	6	3.4	166	2	AB1150	transcription regu	193	6	3.4	245	2	F64465	hypothetical prote
121	6	3.4	166	2	AC1509	weakly transcripti	194	6	3.4	245	2	AB2596	transcription regu
122	6	3.4	167	1	RMGHD3	T-cell surface gly	195	6	3.4	245	2	D97378	histidine utilizat
123	6	3.4	167	2	C86241	protein T1685.9 f1	196	6	3.4	246	1	DEKNG	acetylacetyl-CoA re
124	6	3.4	168	2	T03168	hypothetical prote	197	6	3.4	252	2	PE4047	3-oxoacyl-(acyl)-ca
125	6	3.4	172	2	H83634	conserved hypothet	198	6	3.4	252	2	B83706	hypothetical prote
126	6	3.4	173	1	RMMSD2	T-cell surface gly	199	6	3.4	258	2	G97163	flagellar basal bo
127	6	3.4	173	2	S37960	hypothetical prote	200	6	3.4	259	2	B82029	methionyl aminopep
128	6	3.4	174	2	F95921	glucose-1-phosphat	201	6	3.4	259	2	C81008	hypothetical prote
129	6	3.4	178	2	D82070	conserved hypothet	202	6	3.4	260	1	JKRCT	spore coat-associat
130	6	3.4	178	2	C71686	cytochrome c oxida	203	6	3.4	260	2	C65872	hypothetical prote
131	6	3.4	178	2	B83041	conserved hypothet	204	6	3.4	260	2	B91028	hypothetical prote
132	6	3.4	180	2	AE6321	hypothetical 15.0K	205	6	3.4	260	2	A69881	conserved hypothet
133	6	3.4	181	2	T35851	hypothetical prote	206	6	3.4	261	2	S55010	cytochrome-c oxida
134	6	3.4	182	2	AI3074	conserved hypothet	207	6	3.4	261	2	H69976	hypothetical prote
135	6	3.4	183	2	H98211	hypothetical prote	208	6	3.4	261	2	D69606	spore coat-associat
136	6	3.4	183	2	T18276	hypothetical prote	209	6	3.4	261	2	S72895	hypothetical prote
137	6	3.4	183	2	H97760	hypothetical prote	210	6	3.4	261	2	AC0164	probable transport
138	6	3.4	184	2	S43486	B-cell maturation	211	6	3.4	262	1	OFFP3	cytochrome-c oxida
139	6	3.4	184	2	AC3051	conserved hypothet	212	6	3.4	262	1	OFFP3	cytochrome-c oxida
140	6	3.4	185	2	B64126	hypothetical prote	213	6	3.4	262	1	B64708	conserved hypothet
141	6	3.4	185	2	T12476	hypothetical prote	214	6	3.4	262	1	S69225	conserved hypothet
142	6	3.4	187	2	B83084	probable transcript	215	6	3.4	263	2	G84021	alkylphosphonate A
143	6	3.4	188	2	H97750	cytochrome c oxida	216	6	3.4	265	2	F87668	D-beta-hydroxybuty
144	6	3.4	188	2	F69065	hypothetical prote	217	6	3.4	267	2	AH2362	hypothetical prote
145	6	3.4	189	2	C97476	hypothetical prote	218	6	3.4	267	2	H75429	transcription regu
146	6	3.4	191	2	S74158	hypothetical prote	219	6	3.4	268	2	H71200	agamous-like prote
147	6	3.4	192	2	A64242	GMP-gated cation	220	6	3.4	268	2	C90321	hypothetical prote
148	6	3.4	192	2	S75403	glucose inhibited	221	6	3.4	268	2	D97054	probable membrane
149	6	3.4	193	2	H75508	hypothetical prote	222	6	3.4	271	2	B71277	hypothetical prote
150	6	3.4	194	2	T45625	sensory box protei	223	6	3.4	273	1	B75385	probable ribosomal
151	6	3.4	195	2	T46291	hypothetical prote	224	6	3.4	275	1	S38861	14-3-3 protein hom
152	6	3.4	196	2	I40130	hypothetical prote	225	6	3.4	276	2	T96689	hypothetical prote
153	6	3.4	196	2	D83279	outer surface prot	226	6	3.4	277	1	PSAAB	epidermolitic toxi
154	6	3.4	197	1	WZYVCP	probable transcript	227	6	3.4	278	2	B99415	hypothetical prote
155	6	3.4	197	2	AE1230	G88 protein - she	228	6	3.4	280	2	G83837	hypothetical prote
156	6	3.4	197	2	AE1583	B. subtilis ydei p	229	6	3.4	280	2	T32325	pyrroline-5-carbox
157	6	3.4	198	2	S61585	hypothetical prote	230	6	3.4	282	2	C82490	hypothetical prote
158	6	3.4	198	2	AE2379	hypothetical prote	231	6	3.4	282	2	C82490	probable potassi
159	6	3.4	202	2	D81378	hypothetical prote	232	6	3.4	283	2	D72378	F54F2.8 protein -
160	6	3.4	203	2	UQ1243	probable integral	233	6	3.4	283	2	S72343	sugar ABC transpor
161	6	3.4	203	2	A93865	coat protein I - b	234	6	3.4	283	2	T22618	opacity protein op
162	6	3.4	204	2	I38156	hypothetical prote	235	6	3.4	284	1	RSBST	hypothetical prote
163	6	3.4	204	2	H85753	rho protein GDP-di	236	6	3.4	286	1	T18957	site-specific raco
164	6	3.4	204	2	B86308	partial probable p	237	6	3.4	287	2	S73992	hypothetical prote
165	6	3.4	206	2	S08632	P20D23.10 protein	238	6	3.4	287	2	B87194	ribosomal protein
166	6	3.4	207	2	S21965	nodulin-21 - boye	239	6	3.4	288	2	UQ1136	probable peptidase
167	6	3.4	210	2	T02928	prolactin - silver	240	6	3.4	288	2	T02327	beta-lactamase (EC
168	6	3.4	213	2	AC2379	physical impedance	241	6	3.4	292	2	G83332	nodulin-26 homolog
169	6	3.4	213	2	S54579	hypothetical prote	242	6	3.4	292	2	B84882	probable transcrip
170	6	3.4	214	4	S58320	hypothetical prote	243	6	3.4	293	2	S77254	protein C05D11.9 f
171	6	3.4	220	2	T21811	hypothetical prote	244	6	3.4	293	2	G64592	phosphatidate cycl
172	6	3.4	224	2	T21896	hypothetical prote	245	6	3.4	294	2	AC2915	hypothetical prote
173	6	3.4	224	2	H97232	uncharacterized me	246	6	3.4	295	2	S35914	acyl-CoA thioester
174	6	3.4	224	2	AD1114	thiamin biosynthes	247	6	3.4	297	2	G90564	regulatory protein
175	6	3.4	224	2	AE1475	thiamin biosynthes	248	6	3.4	297	2	H83058	hypothetical prote

249	6	3.4	297	2	ACT1494	322	6	3.4	340	2	S77165	hypothetical prote
250	6	3.4	297	2	A11135	323	6	3.4	341	2	C83067	hypothetical prote
251	6	3.4	298	2	T09921	324	6	3.4	342	2	T04054	protein kinase hom
252	6	3.4	298	2	B90550	325	6	3.4	342	2	T36505	probable ABC-type
253	6	3.4	298	2	B71317	326	6	3.4	343	2	H97057	transcription regu
254	6	3.4	299	2	D95412	327	6	3.4	343	2	D41873	grip 5'-region hea
255	6	3.4	300	1	H70557	328	6	3.4	343	2	H70517	probable lppd prot
256	6	3.4	300	1	P70605	329	6	3.4	343	2	B66468	probable DNA polym
257	6	3.4	300	2	AB1234	330	6	3.4	345	1	QXX12M	NADH2 dehydrogen
258	6	3.4	300	2	AC1597	331	6	3.4	346	2	C72353	hypothetical prote
259	6	3.4	300	2	D70510	332	6	3.4	347	2	T42528	BEH1 protein homol
260	6	3.4	300	2	AE3088	333	6	3.4	347	2	T38998	probable galactosy
261	6	3.4	300	2	E96198	334	6	3.4	347	2	B69952	conserved hypothet
262	6	3.4	302	2	E72402	335	6	3.4	348	1	T26381	purple acid phosph
263	6	3.4	302	2	H69823	336	6	3.4	349	2	E87284	hypothetical prote
264	6	3.4	302	2	AE1067	337	6	3.4	349	2	D84608	hypothetical prote
265	6	3.4	302	2	T38879	338	6	3.4	350	2	B87335	hypothetical prote
266	6	3.4	303	2	D83503	339	6	3.4	351	2	T42421	3-carboxy-cis,cis-
267	6	3.4	303	2	B88990	340	6	3.4	353	2	AF3114	ubiquitine biosynt
268	6	3.4	304	2	A49789	341	6	3.4	353	2	G98172	hypothetical prote
269	6	3.4	304	2	A35001	342	6	3.4	354	2	D71620	hypothetical prote
270	6	3.4	305	2	F95115	343	6	3.4	354	2	S28765	hypothetical prote
271	6	3.4	305	2	T52287	344	6	3.4	355	2	T31780	human microfibrill
272	6	3.4	305	2	A97158	345	6	3.4	355	2	T50093	hypothetical prote
273	6	3.4	306	2	D86805	346	6	3.4	356	1	VVYP2L	coat protein VP2 -
274	6	3.4	306	2	AH2125	347	6	3.4	356	1	E83591	hypothetical prote
275	6	3.4	306	2	T04879	348	6	3.4	357	2	AC1360	protein gp20 (Bact
276	6	3.4	307	2	S56907	349	6	3.4	357	2	B87464	lysophospholipase
277	6	3.4	307	2	P84502	350	6	3.4	358	2	G70026	conserved hypothet
278	6	3.4	308	2	B97002	351	6	3.4	358	2	AE2218	hypothetical prote
279	6	3.4	309	2	T33612	352	6	3.4	359	2	T47987	hypothetical prote
280	6	3.4	310	2	H75153	353	6	3.4	359	2	AB6175	hypothetical prote
281	6	3.4	311	2	C75493	354	6	3.4	360	2	AG2645	flagellar biosynt
282	6	3.4	311	2	B97985	355	6	3.4	360	2	G97427	flhB protein (U951
283	6	3.4	311	2	A57223	356	6	3.4	360	2	H81411	probable periplasm
284	6	3.4	312	2	B75746	357	6	3.4	360	2	T01007	mannose-1-phosphat
285	6	3.4	313	2	E82123	358	6	3.4	361	2	H75260	conserved hypothet
286	6	3.4	313	2	I38176	359	6	3.4	361	2	H70422	G protein-coupled
287	6	3.4	313	2	I84474	360	6	3.4	362	2	I65990	GTP-binding protel
288	6	3.4	314	2	A75258	361	6	3.4	362	2	D84952	mannose-1-phosphat
289	6	3.4	315	2	D71525	362	6	3.4	362	2	T47698	conserved hypothet
290	6	3.4	315	2	A84634	363	6	3.4	364	2	T25309	hypothetical prote
291	6	3.4	316	2	P97689	364	6	3.4	365	2	T36004	hypothetical prote
292	6	3.4	316	2	D90585	365	6	3.4	368	2	G70802	probable PPB prote
293	6	3.4	316	2	G64408	366	6	3.4	369	2	A75166	hypothetical prote
294	6	3.4	318	2	D72050	367	6	3.4	372	2	A70019	optine catabolism h
295	6	3.4	318	2	A86574	368	6	3.4	372	2	T44318	transposase homolo
296	6	3.4	319	2	T26450	369	6	3.4	372	2	I69647	glycosyltransferas
297	6	3.4	320	2	S09208	370	6	3.4	373	2	H84404	ferrichrome ABC tr
298	6	3.4	321	1	J00288	371	6	3.4	373	2	I38177	ras-related GTPase
299	6	3.4	321	1	S58614	372	6	3.4	374	2	S48462	hypothetical prote
300	6	3.4	321	2	H86436	373	6	3.4	377	2	G75095	lps biosynthesis r
301	6	3.4	323	2	C64087	374	6	3.4	377	1	OKXU91	protein kinase (BC
302	6	3.4	324	2	A45752	375	6	3.4	379	2	AE2973	hypothetical prote
303	6	3.4	324	2	T20679	376	6	3.4	379	2	P98309	hypothetical prote
304	6	3.4	325	2	J04950	377	6	3.4	381	1	A60669	protein kinase (BC
305	6	3.4	325	2	TC5276	378	6	3.4	381	1	OKMSR1	benzozate membrane
306	6	3.4	326	2	AD2612	379	6	3.4	383	2	AF3503	hypothetical prote
307	6	3.4	326	2	B97394	380	6	3.4	384	2	P84675	probable membrane
308	6	3.4	327	2	P86813	381	6	3.4	384	2	S64614	alanyl-tRNA synthe
309	6	3.4	329	1	A71511	382	6	3.4	387	2	G97011	alanine racemase (
310	6	3.4	330	2	C83735	383	6	3.4	388	2	H98321	alanine racemase (
311	6	3.4	331	1	A30929	384	6	3.4	388	2	AF2961	hypothetical prote
312	6	3.4	331	2	P85811	385	6	3.4	388	2	H64427	capm protein (capm
313	6	3.4	331	2	AC0752	386	6	3.4	389	2	B71691	major outer membra
314	6	3.4	331	2	P90963	387	6	3.4	389	2	I40864	major outer membra
315	6	3.4	331	2	H64957	388	6	3.4	389	2	D43587	major outer membra
316	6	3.4	331	2	T31779	389	6	3.4	389	2	D86577	major outer membra
317	6	3.4	334	2	T29061	390	6	3.4	389	2	I40739	alanine racemase (
318	6	3.4	335	2	C70196	391	6	3.4	391	2	H97491	alanine racemase (
319	6	3.4	336	2	S06578	392	6	3.4	391	2	AG2709	isoaspartyl dipept
320	6	3.4	339	2	B86281	393	6	3.4	391	2	AG2709	
321	6	3.4	339	2	F82896	394	6	3.4	391	2	A83791	

395	6	3.4	392	2	AH2854	benzoate transport
396	6	3.4	393	2	T04957	hypothetical prote
397	6	3.4	395	2	T23402	conserved hypothet
398	6	3.4	395	2	A69512	hypothetical prote
399	6	3.4	395	2	B83367	two-component sens
400	6	3.4	396	2	Ar2185	hypothetical prote
401	6	3.4	397	2	T25910	pyrimidine nucleos
402	6	3.4	397	2	G70078	hypothetical prote
403	6	3.4	397	2	S74890	conserved hypothet
404	6	3.4	398	2	D83214	conserved hypothet
405	6	3.4	399	2	AR3556	alanine racemase (
406	6	3.4	399	2	T30222	sensory protein Ki
407	6	3.4	400	2	D83892	transcription regu
408	6	3.4	401	2	I39974	serine proteinase
409	6	3.4	401	2	G71564	hypothetical prote
410	6	3.4	404	2	SA2831	F40F12.2 protein -
411	6	3.4	404	2	AR3541	iron-sulfur cluste
412	6	3.4	405	2	AE1002	acetylornithine tr
413	6	3.4	406	2	G86000	acetylornithine de
414	6	3.4	406	2	B91155	acetylornithine de
415	6	3.4	406	2	B65130	acetylornithine tr
416	6	3.4	407	2	C64250	cytosine-cRNA lig
417	6	3.4	408	2	B90517	conserved hypothet
418	6	3.4	411	2	S45142	translacton initia
419	6	3.4	411	2	S75327	lysostaphin - Syle
420	6	3.4	413	1	S16426	cytosine-cRNA lig
421	6	3.4	414	2	T44711	beta-ketocacyl-ACP
422	6	3.4	416	2	AE7116	3-oxoacyl-[acyl]-ca
423	6	3.4	416	2	H69436	5-enolpyruvylshik
424	6	3.4	417	2	T34930	probable secreted
425	6	3.4	419	2	T24820	hypothetical prote
426	6	3.4	419	2	G86517	hypothetical prote
427	6	3.4	420	2	P72103	hypothetical prote
428	6	3.4	420	2	A84492	probable PctA-like
429	6	3.4	421	2	B72573	probable 3-hydroxy
430	6	3.4	422	2	J80239	lin-10 protein - r
431	6	3.4	422	2	B82676	ABC transporter me
432	6	3.4	423	2	T18784	tetracenomycin c p
433	6	3.4	425	2	AC3391	probable RING zinc
434	6	3.4	425	2	AR6849	probable non-proce
435	6	3.4	425	2	C97013	beta-ketocacyl-ACPs
436	6	3.4	426	2	F97552	3-oxoacyl-(acyl)-ca
437	6	3.4	426	2	AH2772	metabolite transpo
438	6	3.4	426	2	C90425	gene hb protein -
439	6	3.4	426	2	I48379	trigger factor (im
440	6	3.4	427	2	B95046	cardoxyl-ferrihal
441	6	3.4	427	2	B97917	hypothetical prote
442	6	3.4	427	2	AS3964	dihydroliopamide S
443	6	3.4	428	2	S50646	probable multiple
444	6	3.4	428	2	AH3536	citrate utilization
445	6	3.4	430	2	A64880	citrate utilization
446	6	3.4	431	1	ZTRC3	citrate utilization
447	6	3.4	431	1	ZTRC6	histidinol dehydro
448	6	3.4	431	2	AB6776	histidinol dehydro
449	6	3.4	431	2	E45734	probable membrane
450	6	3.4	431	2	AF0276	hypothetical prote
451	6	3.4	431	2	T05748	citrate-carrier sym
452	6	3.4	434	2	AR0585	citrate-carrier pr
453	6	3.4	434	2	J00576	hypothetical prote
454	6	3.4	434	2	S62168	glutamy1-cRNA redu
455	6	3.4	436	2	B84329	phosphomannomutase
456	6	3.4	436	2	F69101	glutamy1-cRNA redu
457	6	3.4	437	2	F69496	protein R13D11.3 l
458	6	3.4	437	2	AB8942	transposase for in
459	6	3.4	439	2	B89887	conserved hypothet
460	6	3.4	439	2	F69216	probable penicilli
461	6	3.4	443	2	D95416	glutamate-ammonia
462	6	3.4	444	1	AUBS08	mitosis-specific c
463	6	3.4	445	2	S65734	protein R04F1.3 i
464	6	3.4	445	2	AB8956	replicative DNA he
465	6	3.4	446	2	D64210	hypothetical prote
466	6	3.4	446	2	T16255	hypothetical prote
467	6	3.4	446	2	AB3355	hypothetical prote
468	6	3.4	450	2	C75033	adenylosuccinate 1
469	6	3.4	450	2	T38474	serine-cRNA ligase
470	6	3.4	450	2	E72615	probable hysA APEI
471	6	3.4	450	2	H71135	probable adenylosu
472	6	3.4	451	2	T74954	transducer protein
473	6	3.4	451	2	H84479	probable PctA-like
474	6	3.4	451	2	T16418	hypothetical prote
475	6	3.4	452	2	T38962	hypothetical prote
476	6	3.4	452	2	T40634	hypothetical prote
477	6	3.4	453	2	J80155	mitochondrial inne
478	6	3.4	454	2	AB2572	3-phosphoshikimate
479	6	3.4	454	2	T06363	hypothetical prote
480	6	3.4	454	2	AH3555	atrazine chloronyd
481	6	3.4	457	2	B71476	probable copropor
482	6	3.4	458	2	B64624	GTP-binding protei
483	6	3.4	459	2	S76138	hypothetical prote
484	6	3.4	462	2	E71891	probable GTP bindi
485	6	3.4	463	1	T26378	acid phosphatase (
486	6	3.4	463	2	B83242	probable adenylate
487	6	3.4	464	1	MNVUWC	nonstructural prot
488	6	3.4	465	2	A66679	probable RNA-bind
489	6	3.4	466	2	J06525	processing peptida
490	6	3.4	466	2	AR0190	probable transemb
491	6	3.4	469	2	T49379	citrate synthase,
492	6	3.4	469	2	S41563	citrate (6i)-synth
493	6	3.4	469	2	C70961	hypothetical prote
494	6	3.4	469	2	AR5396	protein (imported
495	6	3.4	470	2	AE7547	vanillin dehydroge
496	6	3.4	470	2	AE2155	hypothetical prote
497	6	3.4	474	2	T06149	hypothetical prote
498	6	3.4	475	2	A10010	probable membrane
499	6	3.4	475	2	AD1497	Bacillus anthracis
500	6	3.4	480	2	F69505	thymidylate synth
501	6	3.4	481	2	D87696	glutamate synthase
502	6	3.4	482	2	D97162	UDP-N-acetylmuram
503	6	3.4	482	2	S44638	hypothetical prote
504	6	3.4	484	2	F89908	gamma-aminobutylat
505	6	3.4	485	2	A71266	probable transcrip
506	6	3.4	485	2	A39408	trk system potassi
507	6	3.4	486	2	S67589	probable membrane
508	6	3.4	487	2	B82065	RNA polymerase sig
509	6	3.4	487	2	B72755	probable antibioci
510	6	3.4	489	1	A53766	phosphonotolide-s
511	6	3.4	490	1	S44545	SSH1 protein - yea
512	6	3.4	490	2	S00995	gene twist protein
513	6	3.4	491	2	T48989	hypothetical prote
514	6	3.4	493	2	T27461	hypothetical prote
515	6	3.4	496	2	A47199	1-aminocyclopropan
516	6	3.4	496	2	E72032	general secretion
517	6	3.4	496	2	F66592	uroporhyrin methy
518	6	3.4	496	2	T41114	hypothetical prote
519	6	3.4	496	2	H83592	hypothetical prote
520	6	3.4	497	2	A53373	trpN protein - Pse
521	6	3.4	497	2	F83087	RNA polymerase sig
522	6	3.4	500	2	AH3424	betaine aldehyde d
523	6	3.4	500	2	C81657	general secretion
524	6	3.4	501	2	F71965	lysine-cRNA ligase
525	6	3.4	501	2	F64542	lysine-cRNA ligase
526	6	3.4	501	2	D71499	probable gen. secr
527	6	3.4	502	2	S00720	transcription init
528	6	3.4	502	2	AD0691	conserved hypothet
529	6	3.4	503	2	B84228	hypothetical prote
530	6	3.4	504	2	AR1789	glucosylase kinase h
531	6	3.4	505	2	C53153	glucose transport
532	6	3.4	508	2	T43154	nitrate transport
533	6	3.4	509	2	AB0683	pyridine nucleotid
534	6	3.4	510	2	AH1811	hypothetical prote
535	6	3.4	511	1	S25707	cytochrome P450 4D
536	6	3.4	511	2	S49151	maturase matk, int
537	6	3.4	511	2	T34315	hypothetical prote
538	6	3.4	512	2	T13611	hypothetical prote
539	6	3.4	512	2	T24032	hypothetical prote
540	6	3.4	512	2	G86459	hypothetical 55.6

541	6	3.4	513	2	T45624	614	6	3.4	615	2	AP2972	rhizobicin secret
542	6	3.4	513	2	T34546	615	6	3.4	615	2	E98310	rhizobicin secret
543	6	3.4	514	2	A81170	616	6	3.4	617	2	B82285	protein-export mem
544	6	3.4	514	2	G81935	617	6	3.4	617	2	T29660	hypothetical prote
545	6	3.4	516	2	E96839	618	6	3.4	617	2	B85044	hypothetical prote
546	6	3.4	520	2	AD2383	619	6	3.4	620	2	T10423	estrogen receptor
547	6	3.4	522	2	S41819	620	6	3.4	620	2	H69382	ABC transporter, A
548	6	3.4	523	2	H70886	621	6	3.4	621	1	D69295	endopeptidase Ia h
549	6	3.4	523	2	T18700	622	6	3.4	621	1	T24090	hypothetical prote
550	6	3.4	524	2	F81207	623	6	3.4	622	2	A45050	transketolase (EC
551	6	3.4	525	2	T20662	624	6	3.4	623	2	P95906	crankshaft adenyate
552	6	3.4	526	2	S03600	625	6	3.4	624	2	A10382	peptidylprolyl iso
553	6	3.4	528	2	T41944	626	6	3.4	628	2	AT0382	topoisomerase IV s
554	6	3.4	528	2	A82256	627	6	3.4	629	2	A82700	hypothetical prote
555	6	3.4	528	2	JC5652	628	6	3.4	630	2	T31798	DNA topoisomerase
556	6	3.4	529	2	D71489	629	6	3.4	632	2	B64127	peptidase PA81418
557	6	3.4	530	2	F84905	630	6	3.4	632	2	E75057	probable SNF2-type
558	6	3.4	530	2	S46589	631	6	3.4	634	2	S32349	dnak protein PA476
559	6	3.4	531	2	D83297	632	6	3.4	637	2	B83052	maltodextrin glyco
560	6	3.4	534	2	JS0173	633	6	3.4	639	2	E72336	beta-glucoside-spe
561	6	3.4	536	2	A34901	634	6	3.4	640	2	AB1422	hypothetical prote
562	6	3.4	536	2	D83419	635	6	3.4	649	2	C81275	phor protein homol
563	6	3.4	539	2	B82393	636	6	3.4	651	2	B84273	leishmanolysin (EC
564	6	3.4	541	2	S46794	637	6	3.4	653	2	A60961	hypothetical prote
565	6	3.4	542	2	B81662	638	6	3.4	653	2	B81277	hypothetical prote
566	6	3.4	542	2	JQ0201	639	6	3.4	653	2	F85620	partial fibrinall u
567	6	3.4	544	2	C95854	640	6	3.4	654	2	AB3553	membrane protein x
568	6	3.4	544	2	S58532	641	6	3.4	660	2	C95287	conserved hypotnet
569	6	3.4	548	2	G70610	642	6	3.4	668	2	C71868	hypothetical prote
570	6	3.4	550	2	H64049	643	6	3.4	673	2	AB1936	hypothetical prote
571	6	3.4	550	2	T22370	644	6	3.4	676	2	AP1153	transcription anti
572	6	3.4	554	2	T41612	645	6	3.4	676	2	T40772	hypothetical prote
573	6	3.4	557	1	DWSPUP	646	6	3.4	681	2	C84612	cell-surface molec
574	6	3.4	557	2	T45008	647	6	3.4	682	2	A49121	connectin precurs
575	6	3.4	559	2	E83007	648	6	3.4	682	2	A43318	hypothetical prote
576	6	3.4	559	2	E89134	649	6	3.4	686	2	T08919	hypothetical prote
577	6	3.4	560	2	G72487	650	6	3.4	688	2	S50580	hypothetical prote
578	6	3.4	563	2	A71513	651	6	3.4	688	2	B42161	hypothetical prote
579	6	3.4	566	2	T31456	652	6	3.4	688	2	S65241	hypothetical prote
580	6	3.4	567	2	T44363	653	6	3.4	689	2	T08918	hypothetical prote
581	6	3.4	569	2	T20702	654	6	3.4	690	2	B42594	D-amino acid hyd
582	6	3.4	569	2	T00851	655	6	3.4	691	2	D84889	probable receptor-
583	6	3.4	570	2	C86440	656	6	3.4	693	2	T39154	probable ABC trans
584	6	3.4	570	2	I45712	657	6	3.4	694	2	AB3396	NADH dehydrogenas
585	6	3.4	573	2	T25397	658	6	3.4	694	2	E82783	hypothetical prote
586	6	3.4	574	2	B83388	659	6	3.4	695	2	A38314	L-amino-acid oxida
587	6	3.4	574	2	S48860	660	6	3.4	699	2	A83375	probable sensor/re
588	6	3.4	575	2	F83904	661	6	3.4	700	2	H82428	iron(III) ABC tran
589	6	3.4	577	2	E71364	662	6	3.4	704	2	S33263	transcription init
590	6	3.4	579	2	T16237	663	6	3.4	704	2	S33263	delta-1-pyrroline-
591	6	3.4	580	1	A34965	664	6	3.4	717	2	S66637	delta-1-pyrroline-5
592	6	3.4	580	1	S15577	665	6	3.4	717	2	T50685	calpain inhibitor
593	6	3.4	581	2	F84657	666	6	3.4	718	1	A26615	hypothetical prote
594	6	3.4	581	2	T31745	667	6	3.4	718	1	A81122	hypothetical prote
595	6	3.4	583	2	I50518	668	6	3.4	719	2	T12258	pyrroline-5-carbox
596	6	3.4	583	2	T32266	669	6	3.4	720	2	A36942	Fe(III)-pyochelin
597	6	3.4	583	2	B82744	670	6	3.4	720	2	A87128	conserved hypotnet
598	6	3.4	585	2	AC3388	671	6	3.4	725	2	UC1300	endo-beta-1,4-glyc
599	6	3.4	586	2	H84966	672	6	3.4	726	2	T47700	delta-1-pyrroline-
600	6	3.4	589	2	NDECS	673	6	3.4	726	2	T50684	pyrroline-5-carbox
601	6	3.4	589	2	T32785	674	6	3.4	727	2	T08920	hypothetical prote
602	6	3.4	589	2	A34341	675	6	3.4	727	2	B83592	hypothetical prote
603	6	3.4	593	1	KIZPMN	676	6	3.4	730	2	S83592	translacton elonga
604	6	3.4	593	1	I46528	677	6	3.4	734	1	S25166	cationic amino aci
605	6	3.4	593	2	E81277	678	6	3.4	736	1	C69451	1,4-alpha-glucan b
606	6	3.4	598	2	E72733	679	6	3.4	741	1	S34218	hypothetical prote
607	6	3.4	599	2	S15789	680	6	3.4	743	1	H96713	hypothetical prote
608	6	3.4	605	2	C71313	681	6	3.4	747	1	VPR4S	outer layer protei
609	6	3.4	609	2	T27397	682	6	3.4	748	2	A64319	carbon-monoxide de
610	6	3.4	609	2	B84783	683	6	3.4	755	2	D75598	photoreceptor - De
611	6	3.4	611	2	T27820	684	6	3.4	761	2	H88429	protein P56F3.1 [l
612	6	3.4	612	2	B55067	685	6	3.4	764	2	S47569	1,4-alpha-glucan b
613	6	3.4	612	2	A97935	686	6	3.4	769	2	T45854	hypothetical prote

687	6	3.4	774	2	T03919	hypothetical prote	760	6	3.4	1118	2	T27865	hypothetical prote
688	6	3.4	775	1	VPXR2	outer layer protei	761	6	3.4	1132	2	T45037	hypothetical prote
689	6	3.4	776	1	VPXR3	outer layer protei	762	6	3.4	1155	2	B96761	probable protein k
690	6	3.4	776	1	VPXR1	outer layer protei	763	6	3.4	1157	2	C96761	hypothetical prote
691	6	3.4	776	2	S24410	hypothetical outer	764	6	3.4	1169	2	C84547	hypothetical prote
692	6	3.4	777	2	S43585	F26F3.1 protein (c	765	6	3.4	1171	2	T00360	hypothetical prote
693	6	3.4	794	2	G81177	phosphoenolpyruvat	766	6	3.4	1176	1	A48047	phospholipase C (B
694	6	3.4	794	2	G81927	probable pyruvate,	767	6	3.4	1177	2	T16594	hypothetical prote
695	6	3.4	794	2	T37989	DNA mismatch repai	768	6	3.4	1180	2	A11939	two-component hycr
696	6	3.4	795	2	T20609	hypothetical prote	769	6	3.4	1180	2	A35854	integrin alpha-1 c
697	6	3.4	801	2	A89862	Na+/H+ antiporter	770	6	3.4	1188	2	T20333	hypothetical prote
698	6	3.4	810	2	S75931	hypothetical prote	771	6	3.4	1200	2	S77524	chromosome segrega
699	6	3.4	815	2	C71810	type I restriction	772	6	3.4	1200	2	C96025	hypothetical expor
700	6	3.4	817	2	C64695	type I restriction	773	6	3.4	1208	2	T27832	hypothetical prote
701	6	3.4	818	2	C69819	endonuclease (imp	774	6	3.4	1214	2	G70953	probable suca prot
702	6	3.4	834	1	MMVXPJ	RNA replicase 2 (E	775	6	3.4	1225	2	T39255	probable C2 domain
703	6	3.4	834	2	T41568	arginonate-like pro	776	6	3.4	1240	2	S52734	hypothetical prote
704	6	3.4	834	2	T03369	hypothetical prote	777	6	3.4	1259	2	T06521	plittylsain (nc 3.4
705	6	3.4	834	2	UC8035	N-acetyltransferas	778	6	3.4	1260	2	A87046	hypothetical prote
706	6	3.4	836	2	T46070	hypothetical prote	779	6	3.4	1279	2	G86684	prophage p11 prote
707	6	3.4	839	2	T45908	hypothetical prote	780	6	3.4	1283	2	T00387	probable p11 prote
708	6	3.4	844	2	I50159	anion transporter	781	6	3.4	1293	2	S42402	xeroderma pigmento
709	6	3.4	844	2	T32608	hypothetical prote	782	6	3.4	1312	2	T30945	probable DNA repai
710	6	3.4	853	2	AD0544	outer membrane fil	783	6	3.4	1314	2	G02870	KIAA0197 protein -
711	6	3.4	854	1	XYBYT1	protein N-acetyltr	784	6	3.4	1324	2	T00386	hypothetical prote
712	6	3.4	856	2	E75292	GCDPF family prote	785	6	3.4	1349	2	T01699	aldehyde oxidase (
713	6	3.4	859	2	AC2089	adenylate cyclase	786	6	3.4	1355	1	VGEBE1	149K glycoprotein
714	6	3.4	860	2	AB2044	adenylate cyclase	787	6	3.4	1358	2	T01698	aldehyde oxidase (
715	6	3.4	862	2	I49583	differentiation an	788	6	3.4	1401	2	T17452	Werner syndrome pr
716	6	3.4	863	2	B72344	tRNA nucleotidyl t	789	6	3.4	1401	2	T30247	Werner syndrome pr
717	6	3.4	866	1	C64834	probable outer mem	790	6	3.4	1401	2	T39225	MAP kinase kinase
718	6	3.4	867	2	T02579	hypothetical prote	791	6	3.4	1421	2	T00333	hypothetical prote
719	6	3.4	870	2	T39731	csx2 protein - fis	792	6	3.4	1428	2	T08852	luciferin A - Califo
720	6	3.4	878	2	I51940	gene VAV2 protein	793	6	3.4	1433	2	B83952	DNA polymerase iii
721	6	3.4	881	2	B82097	protein-P-II uridy	794	6	3.4	1436	2	T14895	DNA helicase 1 - A
722	6	3.4	884	2	T20405	hypothetical prote	795	6	3.4	1460	1	RNB33L	DNA-directed RNA p
723	6	3.4	885	2	S61189	probable membrane	796	6	3.4	1469	2	B36655	slit protein 2 pre
724	6	3.4	891	2	B48642	acortitate hydrat	797	6	3.4	1476	2	AC2220	hypothetical prote
725	6	3.4	895	2	AD0541	outer membrane fil	798	6	3.4	1480	2	A36655	slit protein 1 pre
726	6	3.4	900	2	A81010	phosphoenolpyruvat	799	6	3.4	1488	2	P86428	probable ABC trans
727	6	3.4	902	2	T00588	hypothetical prote	800	6	3.4	1493	2	H71445	hypothetical prote
728	6	3.4	913	2	E75554	valyl-L-RNA synthet	801	6	3.4	1511	2	T42711	sulfonylurea recep
729	6	3.4	916	2	T03323	gene 116 protein -	802	6	3.4	1536	2	A43855	high-molecular-wei
730	6	3.4	917	2	D81953	phosphoenolpyruvat	803	6	3.4	1545	2	T42751	sulfonylurea recep
731	6	3.4	918	2	T21870	hypothetical prote	804	6	3.4	1545	2	T46645	sulfonylurea recep
732	6	3.4	917	2	T02759	hypothetical prote	805	6	3.4	1546	2	T42728	sulfonylurea recep
733	6	3.4	922	2	A30816	band 3 anion trans	806	6	3.4	1568	2	T09074	semaphorin recepto
734	6	3.4	931	2	B75027	hypothetical prote	807	6	3.4	1570	2	T18272	1-phosphatidylinos
735	6	3.4	943	2	S54493	hypothetical prote	808	6	3.4	1592	2	S63208	hypothetical prote
736	6	3.4	951	2	D75377	probable proteinas	809	6	3.4	1597	2	S55144	RLR1 protein - yea
737	6	3.4	965	2	T09846	phosphoenolpyruvat	810	6	3.4	1648	2	S57163	probable membrane
738	6	3.4	983	2	A38224	protein-tyrosine k	811	6	3.4	1661	2	S64800	probable membrane
739	6	3.4	1004	2	T38074	hypothetical prote	812	6	3.4	1759	2	T03725	replicase polyprot
740	6	3.4	1009	2	B89792	hypothetical prote	813	6	3.4	1769	2	S53378	probable membrane
741	6	3.4	1013	1	S04200	NAD ADP-ribosyltra	814	6	3.4	1778	2	T50074	adenylate nucleopor
742	6	3.4	1020	2	T29108	hypothetical prote	815	6	3.4	1839	1	OYBYK	resistance protein
743	6	3.4	1023	2	B38932	phospholipase C (B	816	6	3.4	1847	2	T30558	plexin 3 precursor
744	6	3.4	1029	2	T18925	hypothetical prote	817	6	3.4	1872	2	JC4976	plexin 2 precursor
745	6	3.4	1031	2	H81288	probable sugar tra	818	6	3.4	1884	2	UC4975	plexin B - fruit f
746	6	3.4	1034	2	T30331	P-glycoprotein - T	819	6	3.4	1894	2	UC4980	plexin 1 precursor
747	6	3.4	1036	2	B96682	hypothetical prote	820	6	3.4	1905	2	T15153	plexin - African c
748	6	3.4	1044	2	G98332	rnd multidrug effl	821	6	3.4	1906	2	AD2443	hypothetical prote
749	6	3.4	1044	2	AD2950	RND multidrug effl	822	6	3.4	1945	2	T33937	plexin A - fruit f
750	6	3.4	1050	2	H90316	hypothetical prote	823	6	3.4	1976	2	T56555	sodium channel pro
751	6	3.4	1051	2	S55259	TfR1 protein - mou	824	6	3.4	2025	2	D86201	protein F12K11.6 (
752	6	3.4	1058	2	S65460	apolipoprotein B -	825	6	3.4	2051	2	T33164	plexin B - fruit f
753	6	3.4	1065	2	A43421	SBCE protein - yea	826	6	3.4	2052	2	T18290	FYVE finger-contai
754	6	3.4	1077	2	A96533	probable zinc meta	827	6	3.4	2114	2	E96505	hypothetical prote
755	6	3.4	1086	2	AH1290	cellobiose-phospho	828	6	3.4	2150	2	T08165	RNA1 polyprotein -
756	6	3.4	1086	2	AT1662	cellobiose-phospho	829	6	3.4	2273	2	T09083	hemagglutinin/hemo
757	6	3.4	1101	2	T33153	hypothetical prote	830	6	3.4	2295	2	B71621	probable membrane
758	6	3.4	1103	2	UC4114	Ca2+-transporting	831	6	3.4	2348	2	AD1841	hypothetical prote
759	6	3.4	1107	2	T25450	hypothetical prote	832	6	3.4	2364	2	I40884	cytoxinin L - C1os

833 6 3.4 2366 2 S10317 toxin B - Clostrid  
834 6 3.4 2367 2 S70172 toxin B - Clostrid  
835 6 3.4 2411 2 A46299 tyrosine kinase su  
836 6 3.4 2411 2 D71623 erythrocyte membra  
837 6 3.4 2459 2 AP2136 peptide synthetase  
838 6 3.4 2528 2 T20719 hypothetical prote  
839 6 3.4 2535 2 E59435 myosin IXA (import  
840 6 3.4 2548 2 T30850 fat facets protein  
841 6 3.4 2559 2 T31099 myosin-RhocAP prot  
842 6 3.4 2626 2 S28261 centromere protein  
843 6 3.4 2663 1 S28261 neurofibromin - fr  
844 6 3.4 2764 2 T13949 neurofibromin - fr  
845 6 3.4 2802 2 T13945 neurofibromin - fr  
846 6 3.4 2802 2 T13947 hypothetical prote  
847 6 3.4 2824 2 T22759 hypothetical prote  
848 6 3.4 2911 2 T20566 HD protein - mouse  
849 6 3.4 3119 2 I49729 yersiniabactin bio  
850 6 3.4 3163 2 AB0233 probable polyketid  
851 6 3.4 3163 2 T17440 hypothetical prote  
852 6 3.4 3429 2 T13853 hemagglutinin-like  
853 6 3.4 3442 2 E82589 hemagglutinin-like  
854 6 3.4 3455 2 B82519 CPV protein - midg  
855 6 3.4 3512 2 T17121 hypothetical prote  
856 6 3.4 3514 2 T19997 polyketide synthas  
857 6 3.4 4427 2 PN0637 dynein heavy chain  
858 6 3.4 4639 1 A54794 dynein heavy chain  
859 6 3.4 4644 1 A38905 hypothetical colle  
860 6 3.4 4717 2 T41581

## ALIGNMENTS

RESULT 1  
H83811  
hypothetical protein BH1296 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: H83811  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; PMID:20512582; PMID:11058132  
A/Accession: H83811  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-279 <STO>  
A/Cross-references: UNIPROT:Q9KDB7; GB:AF001511; GB:BA000004; NID:G10173727; PIDN:BA050  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH1296

Query Match 4.5%; Score 8; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFSLLSA 13  
DB 13 LAFSLLSA 20

RESULT 2  
AC2623  
conserved hypothetical protein Atu0379 [imported] - Agrobacterium tumefaciens (strain C58)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AC2623  
R/Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, F.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; PMID:21608550; PMID:11743193  
A/Accession: AC2623  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-305 <KUR>  
A/Cross-references: UNIPROT:Q8UIB8; GB:AE008688; PIDN:AAL41401.1; PID:G17738720; GSPDB:C  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: Atu0379  
A/Map position: circular chromosome

Query Match 4.5%; Score 8; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 3

C97405  
hypothetical protein AGR\_C 664 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: C97405  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Mollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu  
A/Reference number: A97359; PMID:21608551; PMID:11743194  
A/Accession: C97405  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-305 <KUR>  
A/Cross-references: UNIPROT:Q8UIB8; GB:AE007869; PIDN:AKK86196.1; PID:G15155293; GSPDB:C  
C/Genetics:  
A/Gene: AGR\_C 664  
A/Map position: circular chromosome

Query Match 4.5%; Score 8; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 QAAVVKAL 162  
DB 256 QAAVVKAL 263

## RESULT 4

T35259  
probable L-asparagine permease - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: T35259  
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, April 1999  
A/Reference number: Z21573  
A/Accession: T35259  
A/Status: preliminary; translated from GB/EMBL/DD81  
A/Molecule type: DNA  
A/Residues: 1-489 <OLI>  
A/Cross-references: UNIPROT:Q9X7P0; EMBL:AL049587; PIDN:GABA0684.1; GSPDB:GN00070; SCOE  
A/Experimental source: strain A3 (2)  
C/Genetics:  
A/Gene: SCOE:SCSFP2A.17  
A/Map position: arginine permease

Query Match 4.5%; Score 8; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Oy      158 VVKALGEL 165
      |||||
      81 VVKALGEL 88

RESULT 5
T07422
delta 1-pyrroline-5-carboxylate synthetase - tomato
CISpecies: Lycopersicon esculentum (tomato)
CDate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
CAccession: T07422
R:Maggio, A.; Garcia-Rios, M.; Fujita, T.; Bressan, R.A.; Gzonka, L.N.; Joly, R.U.; Hase
Proc. ASPP San Antonio Texas 11, 80, 1996
A>Title: Cloning and partial characterization of PRO2, a second tomato gene encoding the
A:Reference number: Z16027
A:Accession: T07422
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-717 <MAG>
A:Cross-references: UNIPROT:Q96480; EMBL:U60267; NID:g1480669; PID:g1480670
C:Genetics:
A:Gene: PRO2
C:Function:
A:Pathway: proline biosynthesis
C:Superfamily: delta-1-pyrroline-5-carboxylate (P5C) synthetase
C:Keywords: proline biosynthesis

Query Match      4.5%; Score 8; DB 2; Length 717;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      108 KISSILANS 115
      |||||
      365 KISSILANS 372

RESULT 6
A47096
response regulator homolog, aerial mycelium formation - Streptomyces griseus
CISpecies: Streptomyces griseus
CDate: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
CAccession: A47096
R:Ueda, K.; Miyake, K.; Horiouchi, S.; Beppu, T.
J. Bacteriol. 175, 2006-2016, 1993
A>Title: A gene cluster involved in aerial mycelium formation in Streptomyces griseus et
A:Reference number: A47096; MUID:93209944; PMID:8458843
A:Accession: A47096
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <UED>
A:Cross-references: UNIPROT:O07640; GB:DJ3614; NID:g3721543; PIDN:BA33536.1; PID:g30393
C:Superfamily: response regulator with HTM DNA-binding domain, NatL type, response regul
C:Keywords: DNA binding, phosphoprotein
F:154/Binding site: phosphate (Aap) (covalent) #status predicted

Query Match      4.0%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 SLAFSL 11
      |||||
      128 SLAFSL 134

RESULT 7
G84828
hypothetical protein At2g40380 [imported] - Arabidopsis thaliana
CISpecies: Arabidopsis thaliana (mouse-ear cress)
CDate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
CAccession: G84828
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talion, L.
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eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84828
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <STD>
A:Cross-references: UNIPROT:Q961V7; GB:AB002093; NID:g4586054; PIDN:AA025672.1; GSPDB:GN
C:Genetics:
A:Gene: At2g40380
A:Map position: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein T28J14.50

Query Match      4.0%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6 LAFSL 12
      |||||
      90 LAFSL 96

RESULT 8
JC5710
TBP-1 interacting protein - mouse
CISpecies: Mus musculus (house mouse)
CDate: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 09-Jul-2004
CAccession: JC5710
R:Tanaka, T.; Nakamura, T.; Takagi, H.; Sato, M.
Biochem. Biophys. Res. Commun. 239, 176-181, 1997
A>Title: Molecular cloning and characterization of a novel TBP-1 interacting protein (TB
A:Reference number: JC5710; MUID:98005102; PMID:9345291
A:Accession: JC5710
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-217 <TAN>
A:Cross-references: UNIPROT:Q35047; DBJ:AB000121; NID:g2578817; PIDN:BA23155.1; PID:g2
A:Experimental source: testis
C:Comment: This protein is co-localized with Tat binding protein-1 in vivo and enhances
C:Keywords: phosphoprotein
F:200-217/Region: aspartic acid/glutamic acid-rich #status predicted
F:4.28.82/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predict
F:65.163/Binding site: phosphate (Tyr) (covalent) #status predicted
F:80.122.155/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred

Query Match      4.0%; Score 7; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      156 AAAYKAL 162
      |||||
      45 AAAYKAL 51

RESULT 9
G70851
probable gid protein - Mycobacterium tuberculosis (strain H37RV)
CISpecies: Mycobacterium tuberculosis
CDate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
CAccession: G70851
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
J. Conn. R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70851
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-224 <COL>
A:Cross-references: UNIPROT:O53597; GB:AL021426; GB:AL123456; NID:g3261511; PIDN:CA1623
```



A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: gid

Query Match 4.0%; Score 7; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LRRTSL 71  
|||||  
DB 95 LRRTSL 101

RESULT 10  
C75329 conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: C75329  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MID:20036896; PMID:10567266  
A:Accession: C75329

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-241 <NH2>  
A:Cross-references: UNIPROT:Q9RSX2; GB:AE002038; GB:AE000513; MID:g6459790; PIDN:AAF1154  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1999

A:Map position: 1  
C:Superfamily: hypothetical protein b1798

Query Match 4.0%; Score 7; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASLSLARS 9  
|||||  
DB 97 ASLSLARS 103

RESULT 11

T24485 hypothetical protein T05A1.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T24485

R:loyd, C.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19897  
A:Accession: T24485  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-251 <WIL>  
A:Molecule type: DNA  
A:Cross-references: UNIPROT:Q22186; EMBL:Z68219; PIDN:CAA92479.1; GSPDB:GN00022; CESP:TC  
A:Experimental source: clone T05A1  
C:Genetics:  
A:Gene: CESP:T05A1.7  
A:Map position: 4  
A:Introns: 64/2; 107/2; 217/2

Query Match 4.0%; Score 7; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LARSLSL 12  
|||||  
DB 167 LARSLSL 173

RESULT 12

T32329 hypothetical protein C24H12.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T32329

R:Rolling, T.; Wobldmann, P.; Biewald, T.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans coemid C24H12.  
A:Reference number: Z21151  
A:Accession: T32329

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-260 <ROH>  
A:Cross-references: UNIPROT:O17158; EMBL:AF025451; PIDN:AA71202.1; GSPDB:GN00020; CESP.  
A:Experimental source: strain Bristol N2; clone C24H12  
C:Genetics:  
A:Gene: CESP:C24H12.6  
A:Map position: 2  
A:Introns: 31/1; 61/2; 109/2; 136/3; 202/3; 226/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein C24H12.6

Query Match 4.0%; Score 7; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SDRGSV 53  
|||||  
DB 199 SDRGSV 205

RESULT 13

E71674 hypothetical protein RP682 - Rickettsia prowazekii  
C:Species: Rickettsia prowazekii  
C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004

C:Accession: E71674  
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Almark, T.  
Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A:Reference number: A71630; MID:99039499; PMID:9823893  
A:Accession: E71674

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-293 <AND>  
A:Cross-references: UNIPROT:Q9ZCP1; GB:AJ235272; GB:AJ235269; MID:93861033; PIDN:CAA1511  
A:Experimental source: strain Madrid E  
C:Genetics:  
A:Gene: RP682  
C:Superfamily: Mg-dependent DNase, TatD type

Query Match 4.0%; Score 7; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ATNLQEI 42  
|||||  
DB 214 ATNLQEI 220

RESULT 14

A70392 UDP-glucose-4-epimerase - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C:Accession: A70392  
R:Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MID:98196666; PMID:9537320  
A:Accession: A70392

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-327 <AOF>

A:Cross-references: UNIPROT:O67164; GB:AE000721; NID:G2983544; PIDN:AAC07120.1; PID:9298

A:Experimental source: strain VFS

C:Genetics:

A:Gene: galE

C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology F,4-327/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 4.0%; Score 7; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 VKALGE 164

DB 17 VKALGE 23

#### RESULT 15

T04262

mitogen-activated protein kinase kinase (RC 2.7.1.-) 1 [similarity] - Arabidopsis thaliana

N:Alternate names: protein F20B18.180

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C:Accession: T04262

R:Bayan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15263

A:Accession: T04262

A:Molecule type: DNA

A:Residues: 1-354 <BEV>

A:Cross-references: UNIPROT:O04440; EMBL:AL049483

A:Experimental source: cultivar Columbia; BAC clone F20B18

C:Genetics:

A:Gene: MAPKK

A:Map position: 4

A:Introns: 24/2; 52/3; 97/3; 172/3; 233/3; 308/2; 323/3

A>Note: F20B18.180

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: phosphotransferase

Query Match 4.0%; Score 7; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 SSLANSF 116

DB 219 SSLANSF 225

Search completed: November 2, 2005, 19:01:49  
Job time : 66 secs